



[illegible]

Qy	2581	AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCCTGTGCCCTT	2640
Db	2581	AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCCTGTGCCCTT	2640
Qy	2641	GAAGAGATTGGGAGGACACACACGAAATCTCTCAACATTTTCAGAAATCCCGACTTTGATGA	2700
Db	2641	GAAGAGATTGGGAGGACACACACGAAATCTCTCAACATTTTCAGAAATCCCGACTTTGATGA	2700
Qy	2701	GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG	2736
Db	2701	GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG	2736

RESULT 2  
 US-09-969-532-33  
 ; Sequence 33, Application US/09969532  
 ; Patent No. 6777232  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; APPLICANT: Scoville, John  
 ; TITLE OF INVENTION: No. 6777232a1 Human Membrane Proteins and Polynucleotide  
 ; FILE REFERENCE: LEX-0244-USA  
 ; CURRENT APPLICATION NUMBER: US/09/969,532  
 ; CURRENT FILING DATE: 2001-10-02  
 ; PRIOR APPLICATION NUMBER: US 60/237,280  
 ; PRIOR FILING DATE: 2000-10-02  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 33  
 ; LENGTH: 3411  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-09-969-532-33

Query Match	100.0%	Score	2736;	DB	4;	Length	3411;
Best Local Similarity	100.0%	Pred.	No. 0;				
Matches	2736;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	ATGGGGGAGAGCGGCGGCACCGCAGGCGGGCGGGCGGAGGGGCGCGCGCTGGCTCCCTGG	60				
Db	115	ATGGGGGAGAGCGGCGGCACCGCAGGCGGGCGGGCGGAGGGGCGCGCGCTGGCTCCCTGG	174				
Qy	61	CTGGGGCTGTGCTTCTGGGGCGCAGGGACCGCGGCTGCCCGAGGAACTGACAAATGGCGAA	120				
Db	175	CTGGGGCTGTGCTTCTGGGGCGCAGGGACCGCGGCTGCCCGAGGAACTGACAAATGGCGAA	234				
Qy	121	GCCCTTCCGGAATCCATCCCATCAGCTCCTGGGACACTGCGCTCATTTTCATAGAGAGCCA	180				
Db	235	GCCCTTCCGGAATCCATCCCATCAGCTCCTGGGACACTGCGCTCATTTTCATAGAGAGCCA	294				
Qy	181	GATGATGCTTATATTATCAAGAGCAACCCATTATGCATCTCAGGTGCAAAGCGAGGCCAGCC	240				
Db	295	GATGATGCTTATATTATCAAGAGCAACCCATTATGCATCTCAGGTGCAAAGCGAGGCCAGCC	354				
Qy	241	ATGCAGATATTTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGACAGCTCTCTGAA	300				
Db	355	ATGCAGATATTTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGACAGCTCTCTGAA	414				
Qy	301	GAGACTCTGGACGAGAGCTCAGGTTTGAAGTCCGCGAAGTGTTCATCAATGTTACTAGG	360				
Db	415	GAGACTCTGGACGAGAGCTCAGGTTTGAAGTCCGCGAAGTGTTCATCAATGTTACTAGG	474				
Qy	361	CAACAGGTGGAGGACTTCCATGSGCCGAGGACATATTGGTSCCAGTGTGTGGCGCTGGAGC	420				
Db	475	CAACAGGTGGAGGACTTCCATGSGCCGAGGACATATTGGTSCCAGTGTGTGGCGCTGGAGC	534				
Qy	421	CACCTGGGTACTCTCCAGAGCAGGAAGGCCTCTGTGGGCATAGCCTATTTTACGGAAGAAC	480				
Db	535	CACCTGGGTACTCTCCAGAGCAGGAAGGCCTCTGTGGGCATAGCCTATTTTACGGAAGAAC	594				
Qy	481	TTTGAACAAGACCCCAAGGAAGGGAAGTTCCCATTTGAAGGCATGATTGTATCTGCATGC	540				

Db	595	TTTGAACAAGACCCACAAGGAAGTTCCCATTTGACGGCATGATTTGACTGCACTGC	654
Qy	541	CGCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCAATT	600
Db	655	CGCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCAATT	714
Qy	601	GACTCTGAAACAAGACGAGAACATTTGACACAGAGGCTGACCATTAACCTGATCATCAGGCAG	660
Db	715	GACTCTGAACAAGAAGAGAACATTTGACACAGAGGCTGACCATTAACCTGATCATCAGGCAG	774
Qy	661	GCACGGCTCTCGAGCTCAGGAAATTAACACCTGCATGGCAGCCAACTCGTGGCTTAAGAGG	720
Db	775	GCACGGCTCTCGAGCTCAGGAAATTAACACCTGCATGGCAGCCAACTCGTGGCTTAAGAGG	834
Qy	721	AGAAGCCTGCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA	780
Db	835	AGAAGCCTGCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA	894
Qy	781	TGGTCCGTCTGCAGTCCAGAGTGTGAACAATTTGGGATCCGGAGTGCACAGACACACCC	840
Db	895	TGGTCCGTCTGCAGTCCAGAGTGTGAACAATTTGGGATCCGGAGTGCACAGACACACCC	954
Qy	841	CCGAGAAATCGGGGCAAAATTTCTGTGAAGTCTAAGCCAGGAATCTGAARACTGCACAGAT	900
Db	955	CCGAGAAATCGGGGCAAAATTTCTGTGAAGTCTAAGCCAGGAATCTGAARACTGCACAGAT	1014
Qy	901	GGTCTTTGCACTCTAGATAAAAAACCTCTTCATGAATAAAAAACCCAAAGCATTTGAGAAT	960
Db	1015	GGTCTTTGCACTCTAGATAAAAAACCTCTTCATGAATAAAAAACCCAAAGCATTTGAGAAT	1074
Qy	961	GCACGACAAATGCTTTGTACTCGGGTCTGGGTGCTGCCGTGCTGGCCGTTGCAGTCTCTG	1020
Db	1075	GCACGACAAATGCTTTGTACTCGGGTCTGGGTGCTGCCGTGCTGGCCGTTGCAGTCTCTG	1134
Qy	1021	GTCAATGGTGTCAACCTTTACAGACGGAGCCAGGTGACTATGGCGTGGAGCTCATTTGAC	1080
Db	1135	GTCAATGGTGTCAACCTTTACAGACGGAGCCAGGTGACTATGGCGTGGAGCTCATTTGAC	1194
Qy	1081	TCCTTCTGCAATGACAGTGGCTTCCAGACCTTCAAATTTCAAAAACAGTCCCGTCAAGCCAAAG	1140
Db	1195	TCCTTCTGCAATGACAGTGGCTTCCAGACCTTCAAATTTCAAAAACAGTCCCGTCAAGCCAAAG	1254
Qy	1141	AATATCATGAACTAATGATACAGAAAAATTCCTTTGGTAACCTCCCTGCTCCTGAAATCTCT	1200
Db	1255	AATATCATGAACTAATGATACAGAAAAATTCCTTTGGTAACCTCCCTGCTCCTGAAATCTCT	1314
Qy	1201	GCCATGACGCCAGATCTGACAGTGAGCCGACACATACAGCCGACCCACTCTGCTGCGAGAC	1260
Db	1315	GCCATGACGCCAGATCTGACAGTGAGCCGACACATACAGCCGACCCACTCTGCTGCGAGAC	1374
Qy	1261	CCCTGGAACAAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTTGTGCGGACATCAAA	1320
Db	1375	CCCTGGAACAAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTTGTGCGGACATCAAA	1434
Qy	1321	GTGAAAGTCCAGAGCTCGTTTCATGGTTTCCTCGGAGTGTCTGAGAGAGCTGAGTACCAC	1380
Db	1435	GTGAAAGTCCAGAGCTCGTTTCATGGTTTCCTCGGAGTGTCTGAGAGAGCTGAGTACCAC	1494
Qy	1381	GGCAAGAAATCAATTCAGGACTTTTCCCCATGGAAACAAACACAGCTTTTAGTACAAATGCAT	1440
Db	1495	GGCAAGAAATCAATTCAGGACTTTTCCCCATGGAAACAAACACAGCTTTTAGTACAAATGCAT	1554
Qy	1441	CCCAAGAAATAAAATGCCCTACATCAAAAATCTGTTCATCACTCCCAACAGACAGCAACTG	1500
Db	1555	CCCAAGAAATAAAATGCCCTACATCAAAAATCTGTTCATCACTCCCAACAGACAGCAACTG	1614
Qy	1501	AGGACAACTGGTGTCTTTTGGCCATTTAGGGGGGGCGCTTAGTAAATGCCAAAATACAGGGGTG	1560
Db	1615	AGGACAACTGGTGTCTTTTGGCCATTTAGGGGGGGCGCTTAGTAAATGCCAAAATACAGGGGTG	1674
Qy	1561	AGCTTACTCATACACACGGTGCCATCCCAAGAGAAATTTCTGGGAGATTTATATATGTGCC	1620
Db	1675	AGCTTACTCATACACACGGTGCCATCCCAAGAGAGAAATTTCTGGGAGATTTATATATGTGCC	1734

1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGTGCTCTGAGTCTCTGAA 1680  
 1735 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGTGCTCTGAGTCTCTGAA 1794  
 1681 GTCACTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTTGGCATTTGACCAATCCCGCAC 1740  
 1795 GTCACTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTTGGCATTTGACCAATCCCGCAC 1854  
 1741 TGTGCAGATGTGAGTCTGAGCAATGGAAATATCCATTTAAAGAAAGGACACACAGAGGCG 1800  
 1855 TGTGCAGATGTGAGTCTGAGCAATGGAAATATCCATTTAAAGAAAGGACACACAGAGGCG 1914  
 1801 AAATGGAGGAAGTGTGAGTGGAGAGTGTACATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
 1915 AAATGGAGGAAGTGTGAGTGGAGAGTGTACATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1974  
 1861 CCCTTTGCGGTGTCATGTGCTGCTGCGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920  
 1975 CCCTTTGCGGTGTCATGTGCTGCTGCGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 2034  
 1921 ATCAAGACGTGCGGTGGAAGCAACTGAAGTGGGCGGTTTTGGCTGCGATGCTCTGTAAC 1980  
 2035 ATCAAGACGTGCGGTGGAAGCAACTGAAGTGGGCGGTTTTGGCTGCGATGCTCTGTAAC 2094  
 1981 TCCCTGGATTTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCTATTTCAAGGAA 2040  
 2095 TCCCTGGATTTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCTATTTCAAGGAA 2154  
 2041 GTGGTTTTCAGATGAAGGCACTCAAGGTGGACAGCTCTCTGGAAGAACAAATTTGCTGCAAT 2100  
 2155 GTGGTTTTCAGATGAAGGCACTCAAGGTGGACAGCTCTCTGGAAGAACAAATTTGCTGCAAT 2214  
 2101 TTCAAGAGGAATACCTTTAGTCTTCAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
 2215 TTCAAGAGGAATACCTTTAGTCTTCAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2274  
 2161 AGAATTAACCACTTCACTGCTGCGAGGAGTCCCGTTCTCCGCGGTGTGGTGCAGTAAC 2220  
 2275 AGAATTAACCACTTCACTGCTGCGAGGAGTCCCGTTCTCCGCGGTGTGGTGCAGTAAC 2334  
 2221 CGGAGCGCCCTGCACTGTGCTTTCTCCCTGGAGCGTTTATACGCCCACTACCAACCCAGCTG 2280  
 2335 CGGAGCGCCCTGCACTGTGCTTTCTCCCTGGAGCGTTTATACGCCCACTACCAACCCAGCTG 2394  
 2281 TCCTGCAAAATCTGCAATTCGGAGCTCAAGGCCATGAACAGATCTCTCAAGTGCAGACA 2340  
 2395 TCCTGCAAAATCTGCAATTCGGAGCTCAAGGCCATGAACAGATCTCTCAAGTGCAGACA 2454  
 2341 TCAATCTAGAGGTGAACGAGAAACCATCACTTTCTTTCGCAACAGAGGACAGCACTTTC 2400  
 2455 TCAATCTAGAGGTGAACGAGAAACCATCACTTTCTTTCGCAACAGAGGACAGCACTTTC 2514  
 2401 CCTGCAAGCTGGCCCCCAAGCCTTCAAAATTTCCCTACTCTCAATCAAGAGAGAGTTGT 2460  
 2515 CCTGCAAGCTGGCCCCCAAGCCTTCAAAATTTCCCTACTCTCAATCAAGAGAGAGTTGT 2574  
 2461 GCTACATTTGATACCCCAATGCAAGGCAAGGCTGGCAGATGTTAGCACAGAAAC 2520  
 2575 GCTACATTTGATACCCCAATGCAAGGCAAGGCTGGCAGATGTTAGCACAGAAAC 2634  
 2521 AGCATCAACAGGAATTTATCTTATTTGCTACCAAAAGTAGCCCATCTGCTGCTATTTTG 2580  
 2635 AGCATCAACAGGAATTTATCTTATTTGCTACCAAAAGTAGCCCATCTGCTGCTATTTTG 2694  
 2581 AACCTGGAAGCTGCTGATCAAGAGATGATGTTGATCTTCACTCCCTGGGCTGTGGCCTT 2640  
 2695 AACCTGGAAGCTGCTGATCAAGAGATGATGTTGATCTTCACTCCCTGGGCTGTGGCCTT 2754  
 2641 GAAGAGATTTGGAGGACACACAGAACTCTCAAACTTTTCAAGATCCCAAGCTTGTATGAA 2700  
 2755 GAAGAGATTTGGAGGACACACAGAACTCTCAAACTTTTCAAGATCCCAAGCTTGTATGAA 2814

2701 GCCGACTTCAACTACAGCAGGCAAAATGACTCTAG 2736  
 2815 GCCGACTTCAACTACAGCAGGCAAAATGACTCTAG 2850  
 RESULT 3  
 US-09-969-532-11  
 ; Sequence 11, Application US/09969532  
 ; Patent No. 677222  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; APPLICANT: Scoville, John  
 ; TITLE OF INVENTION: No. 677232el Human Membrane Proteins and Polynucleotides Encodi  
 ; FILE REFERENCE: LEX-0244-USA  
 ; CURRENT APPLICATION NUMBER: US/09/969,532  
 ; PRIOR FILING DATE: 2001-10-02  
 ; PRIOR APPLICATION NUMBER: US 60/237,280  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 11  
 ; LENGTH: 2703  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-969-532-11  
 Query Match 97.2%; Score 2660; DB 4; Length 2703;  
 Best Local Similarity 98.8%; Pred. No. 0;  
 Matches 2703; Conservative 0; Mismatches 0; Indels 33; Gaps 1;  
 1 ATGGGGAGAGCGCGGCCACCGCAGCGCGCGGAGGGCGCGCGCTGGTGGTCCCGTGG 60  
 1 ATGGGGAGAGCGCGGCCACCGCAGCGCGCGGAGGGCGCGCGCTGGTGGTCCCGTGG 60  
 61 CTGGGGCTGTGCTTCTGGGGCGGAGGACCGCGGCTGCCCGAGGAACCTGACAAATGGCGAA 120  
 61 CTGGGGCTGTGCTTCTGGGGCGGAGGACCGCGGCTGCCCGAGGAACCTGACAAATGGCGAA 120  
 121 GCCCTTCCGGAATCCATCCATCAGCTCCTGGGACACTGCTCTCATTTATAGAGAGCCA 180  
 121 GCCCTTCCGGAATCCATCCATCAGCTCCTGGGACACTGCTCTCATTTATAGAGAGCCA 180  
 181 GATGATGCTTATTTATTAAGAGCAACCTTATTTGCACTCAGGTGCAAGCGAGGCGCAGCC 240  
 181 GATGATGCTTATTTATTAAGAGCAACCTTATTTGCACTCAGGTGCAAGCGAGGCGCAGCC 240  
 241 ATGCAAGATTTCTTCAAAATGCAACCGCGAGTGGGTCCATCAGAACGAGCACGCTCTGAA 300  
 241 ATGCAAGATTTCTTCAAAATGCAACCGCGAGTGGGTCCATCAGAACGAGCACGCTCTGAA 300  
 301 GAGACTCTGAGAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTTACTAGG 360  
 301 GAGACTCTGAGAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTTACTAGG 360  
 361 CAACAGGTGGAGACTTCCATGGGCCCGAGGACTATTTGGTGCAGTGTGGGTGGAGC 420  
 361 CAACAGGTGGAGACTTCCATGGGCCCGAGGACTATTTGGTGCAGTGTGGGTGGAGC 420  
 421 CACCTGGGTACCTTCCAAAGAGCAGGAGGCTCTGTGCGCATAGCTTATTTACGAAAGAAC 480  
 421 CACCTGGGTACCTTCCAAAGAGCAGGAGGCTCTGTGCGCATAGCTTATTTACGAAAGAAC 480  
 481 TTTGAAACAAGACCCACAGGAAAGGAAAGTTCCCATTTGAAGGCATGATTGCTGCACTGC 540  
 481 TTTGAAACAAGACCCACAGGAAAGGAAAGTTCCCATTTGAAGGCATGATTGCTGCACTGC 540  
 541 CGCCCAACAGAGGAGTCCCTGCTGCGAGGTGGAAATGCTGAAATGAAGGCCCATTT 600  
 541 CGCCCAACAGAGGAGTCCCTGCTGCGAGGTGGAAATGCTGAAATGAAGGCCCATTT 600  
 601 GACTCTGAAACAGACAGAGAACATTGACACAGGCGCTGACCATAACTGATCATCAGGCAG 660  
 601 GACTCTGAAACAGACAGAGAACATTGACACAGGCGCTGACCATAACTGATCATCAGGCAG 660



QY 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGATGCGACGCCAACATCGTGGCTAAGAGG 720  
 Db 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGATGCGACGCCAACATCGTGGCTAAGAGG 720  
 QY 721 AGAAGCCTGTGGCCACTGTGTGGTCTACGTGATGGAGCTGGGAAGTGTGGAGGAA 780  
 Db 721 AGAAGCCTGTGGCCACTGTGTGGTCTACGTGATGGAGCTGGGAAGTGTGGAGGAA 780  
 QY 781 TGGTCCGTCTGCAAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGACCAACC 840  
 Db 781 TGGTCCGTCTGCAAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGACCAACC 840  
 QY 841 CCGAGAAATCGGGGCAAAATTCGTGAAGGTCTAAGCCAGGAATCTGAAAATCTGCACAGAT 900  
 Db 841 CCGAGAAATCGGGGCAAAATTCGTGAAGGTCTAAGCCAGGAATCTGAAAATCTGCACAGAT 900  
 QY 901 GGTCTTTGCAATCTAGATAAAAAACCTTTTCATGAATAAACCACCAAGCAATTTGAGAAAT 960  
 Db 901 GGTCTTTGCAATCTAG-----GCAATTTGAGAAAT 927  
 QY 961 GCCAGGCAATTTGTTGTAATCGGGCTTGGGTCTGCGCTGCTGGCGGTGCGAGTCTG 1020  
 Db 928 GCCAGGCAATTTGTTGTAATCGGGCTTGGGTCTGCGCTGCTGGCGGTGCGAGTCTG 987  
 QY 1021 GTCAATGGTGTCAACCTTTTACAGCGAGGCCAGAGTGAATGATGGCGTGGACGTCATTGAC 1080  
 Db 988 GTCAATGGTGTCAACCTTTTACAGCGAGGCCAGAGTGAATGATGGCGTGGACGTCATTGAC 1047  
 QY 1081 TCTTTCTGCAATGACAGTGGCTTCCAGACCTTCAACTTTCAAAACAGTCCGCTCAAGCCAG 1140  
 Db 1048 TCTTTCTGCAATGACAGTGGCTTCCAGACCTTCAACTTTCAAAACAGTCCGCTCAAGCCAG 1107  
 QY 1141 AATATCATGAACTAATGATACAGGAAATTCCTTTGGTAACTCCCTGCTCTCTGAAATTC 1200  
 Db 1108 AATATCATGAACTAATGATACAGGAAATTCCTTTGGTAACTCCCTGCTCTCTGAAATTC 1167  
 QY 1201 GCCATGAGCCAGATCTGACAGTGGCGGACATACAGCGGACCCATCTGTCTGCGAGGAC 1260  
 Db 1168 GCCATGAGCCAGATCTGACAGTGGCGGACATACAGCGGACCCATCTGTCTGCGAGGAC 1227  
 QY 1261 CCTCTGACAAAGAGCTCATGACAGAGTCTCTACTCTTTAAACCTTTGTCGGACATCAA 1320  
 Db 1228 CCTCTGACAAAGAGCTCATGACAGAGTCTCTACTCTTTAAACCTTTGTCGGACATCAA 1287  
 QY 1321 GTGAAAGTCCAGAGCTCGTTTCATGTTTCCCTGGAGTGTCTGAGAGCTGAGTACAC 1380  
 Db 1288 GTGAAAGTCCAGAGCTCGTTTCATGTTTCCCTGGAGTGTCTGAGAGCTGAGTACAC 1347  
 QY 1381 GGCAGAAATCAATTCAGGACTTTTCCCATGGAACAAACCAAGCTTTAGTACAATGTCAT 1440  
 Db 1348 GGCAGAAATCAATTCAGGACTTTTCCCATGGAACAAACCAAGCTTTAGTACAATGTCAT 1407  
 QY 1441 CCCAGAAATCAATTCAGGACTTTTCCCATGGAACAAACCAAGCTTTAGTACAATGTCAT 1500  
 Db 1408 CCCAGAAATCAATTCAGGACTTTTCCCATGGAACAAACCAAGCTTTAGTACAATGTCAT 1467  
 QY 1501 AGGACAACTGCTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560  
 Db 1468 AGGACAACTGCTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1527  
 QY 1561 AGCTTACTCATACACAGGTGCCATCCAGAGAGAAATCTTGGGAGATTTATATGTCC 1620  
 Db 1528 AGCTTACTCATACACAGGTGCCATCCAGAGAGAAATCTTGGGAGATTTATATGTCC 1587  
 QY 1621 ATCAACCAAGGTGAAACCGCTTCCAGTCAAGTGGCTCTGAGTGTCTCTGAGTCTCTGAA 1680  
 Db 1588 ATCAACCAAGGTGAAACCGCTTCCAGTCAAGTGGCTCTGAGTGTCTCTGAGTCTCTGAA 1647  
 QY 1681 GTCACTGTGGTCTCCAGACATGATCGTCAACACTCCCTTTGCAATGACCATCCCGCAC 1740  
 Db 1648 GTCACTGTGGTCTCCAGACATGATCGTCAACACTCCCTTTGCAATGACCATCCCGCAC 1707

RESULT 4  
 US-09-969-532-13  
 ; Sequence 13, Application US/09969532  
 ; Patent No. 6777232

QY 1741 TGTGCAAGTGTCTGAGCTTGGATATCCATTTAAGAGAGGACACAGCAGGC 1800  
 Db 1708 TGTGCAAGTGTCTGAGCTTGGATATCCATTTAAGAGAGGACACAGCAGGC 1767  
 QY 1801 AAATGGAGGAACTGATGTCTGAGTGAAGTGAATCTACATCTCTGTACTGCTTTTGGAC 1860  
 Db 1768 AAATGGAGGAACTGATGTCTGAGTGAAGTGAATCTACATCTCTGTACTGCTTTTGGAC 1827  
 QY 1861 CCCTTTGCGGTCTCATGTCTCTGGAAGCTTTGGGACCTATGCGCTCACTGAGAGGCCA 1920  
 Db 1828 CCCTTTGCGGTCTCATGTCTCTGGAAGCTTTGGGACCTATGCGCTCACTGAGAGGCCA 1887  
 QY 1921 ATCAACAGCTGTGCGCTGAGCAACTGAAAGTGGCGGTTTTTGGCTGCATGCTCTGTAAC 1980  
 Db 1888 ATCAACAGCTGTGCGCTGAGCAACTGAAAGTGGCGGTTTTTGGCTGCATGCTCTGTAAC 1947  
 QY 1981 TCCTCTGATTTACAACTTTGAGAGTTTACTGTGTGGAACAATACCCCTTTGTGATTTTCAGGAA 2040  
 Db 1948 TCCTCTGATTTACAACTTTGAGAGTTTACTGTGTGGAACAATACCCCTTTGTGATTTTCAGGAA 2007  
 QY 2041 GTGGTTTCAGATGAAAGGCAATCAAGGTGGACAGCTCTCTGGAAGAACCAAAATTTGCTGCAT 2100  
 Db 2008 GTGGTTTCAGATGAAAGGCAATCAAGGTGGACAGCTCTCTGGAAGAACCAAAATTTGCTGCAT 2067  
 QY 2101 TTCAAAGGGNATACCTTTTAGTCTTTCAGATTTCTGCTCTGATATTTCCCTCTCTGG 2160  
 Db 2068 TTCAAAGGGNATACCTTTTAGTCTTTCAGATTTCTGCTCTGATATTTCCCTCTCTGG 2127  
 QY 2161 AGAATTTAAACCAATTTCACTGCTGCCAGGAAGTCCCGTTCTCCCGGTGTGGTGCAGTAAC 2220  
 Db 2128 AGAATTTAAACCAATTTCACTGCTGCCAGGAAGTCCCGTTCTCCCGGTGTGGTGCAGTAAC 2187  
 QY 2221 CGGACGCCCTGCACTGTGCTCTCTCTGAGAGCTTATACGCCCACTACCAACCCAGCTG 2280  
 Db 2188 CGGACGCCCTGCACTGTGCTCTCTCTGAGAGCTTATACGCCCACTACCAACCCAGCTG 2247  
 QY 2281 TCTGCAAAATCTGCAATTCGGGAGCTCAAGGCGCATGACAGATCTCTCAAGTGCAGACA 2340  
 Db 2248 TCTGCAAAATCTGCAATTCGGGAGCTCAAGGCGCATGACAGATCTCTCAAGTGCAGACA 2307  
 QY 2341 TCAATCTGAGAGTGAACGAGAAACCATCACTTTCTTTCGCAACAAGAGGACAGCACTTTC 2400  
 Db 2308 TCAATCTGAGAGTGAACGAGAAACCATCACTTTCTTTCGCAACAAGAGGACAGCACTTTC 2367  
 QY 2401 CTTGCA CAGACTGCCCCCAAGCCTTCAAATTTCCCTACTCTCATGACAGCGGATTTGT 2460  
 Db 2368 CTTGCA CAGACTGCCCCCAAGCCTTCAAATTTCCCTACTCTCATGACAGCGGATTTGT 2427  
 QY 2461 GCTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCAGAGAAAAC 2520  
 Db 2428 GCTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCAGAGAAAAC 2487  
 QY 2521 AGCATCAACAGGAAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCTGCTGATTTTG 2580  
 Db 2488 AGCATCAACAGGAAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCTGCTGATTTTG 2547  
 QY 2581 AACCTGTGGAGAGCTCTCATCTGATGATGTTGATCTTTCGCTCTCTGCTGCTGCTG 2640  
 Db 2548 AACCTGTGGAGAGCTCTCATCTGATGATGTTGATCTTTCGCTCTCTGCTGCTGCTG 2607  
 QY 2641 GAAGAGATTTGGGAGGACACACAGAAACTCTCAACATTTTCAGATCCAGAGCTTGATGAA 2700  
 Db 2608 GAAGAGATTTGGGAGGACACACAGAAACTCTCAACATTTTCAGATCCAGAGCTTGATGAA 2667  
 QY 2701 GCGGACTTCAACTACAGCAGGCAAAATGGAATCTAG 2736  
 Db 2668 GCGGACTTCAACTACAGCAGGCAAAATGGAATCTAG 2703

GENERAL INFORMATION:  
 APPLICANT: Walke, D. Wade  
 APPLICANT: Scoville, John  
 TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodir  
 FILE REFERENCE: LEX-0244-USA  
 CURRENT APPLICATION NUMBER: US/09/969,532  
 CURRENT FILING DATE: 2001-10-02  
 PRIOR APPLICATION NUMBER: US 60/237,280  
 PRIOR FILING DATE: 2000-10-02  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 13  
 LENGTH: 2694  
 TYPE: DNA  
 ORGANISM: homo sapiens  
 US-09-969-532-13

Query Match 96.6%; Score 2642; DB 4; Length 2694;  
 Best Local Similarity 98.5%; Pred. No. 0;  
 Matches 2694; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY	1	ATGGGAGAGCGCGGCCACCGCAGGGCGGGCGGAGGGCGCGCGCTCCCGTGG	60
DB	1	ATGGGAGAGCGCGGCCACCGCAGGGCGGGCGGAGGGCGCGCGCTCCCGTGG	60
QY	61	CTGGGCTGTCTTCTGGGCGGCGAGGACCGCGCGCTGCCCGAGGAACTGACAAATGCGGAA	120
DB	61	CTGGGCTGTCTTCTGGGCGGCGAGGACCGCGCGCTGCCCGAGGAACTGACAAATGCGGAA	120
QY	121	GCCTTTCCGAAATCCATCCCATCAGTCTCTGGGACACTGCTCATTTCTAGAGGAGCCA	180
DB	121	GCCTTTCCGAAATCCATCCCATCAGTCTCTGGGACACTGCTCATTTCTAGAGGAGCCA	180
QY	181	GATGATGCTTATATATCAAGAGCAACCCCTATTGCACTCAGGTGCAAGCGGCCAGCC	240
DB	181	GATGATGCTTATATATCAAGAGCAACCCCTATTGCACTCAGGTGCAAGCGGCCAGCC	240
QY	241	ATGCAGATATCTTCAAAATGCAACGGCGAGTGGTCCATCAGAACGAGCAGCTCTCTGAA	300
DB	241	ATGCAGATATCTTCAAAATGCAACGGCGAGTGGTCCATCAGAACGAGCAGCTCTCTGAA	300
QY	301	GAGACTCTGACGAGAGCTCAGTTTGAAGTTCGGAGTTCGAGTGTTCATATGTTACTAGG	360
DB	301	GAGACTCTGACGAGAGCTCAGTTTGAAGTTCGGAGTTCGAGTGTTCATATGTTACTAGG	360
QY	361	CAACAGTGGAGGACTTCCATGGCCCGAGGACTATTGGTCCAGTGTGTGGGCTGGAGC	420
DB	361	CAACAGTGGAGGACTTCCATGGCCCGAGGACTATTGGTCCAGTGTGTGGGCTGGAGC	420
QY	421	CACCTGGGTACCTCCAAAGACGAGGAGGCTCTGTGGCAGTACCTATTTCAGGAAAC	480
DB	421	CACCTGGGTACCTCCAAAGACGAGGAGGCTCTGTGGCAGTACCTATTTCAGGAAAC	480
QY	481	TTTGAACAGACCCACAGGAGGAGTTCCTTGAAGGATGCAATGAGGATGTTACTGCACTGC	540
DB	481	TTTGAACAGACCCACAGGAGGAGTTCCTTGAAGGATGCAATGAGGATGTTACTGCACTGC	540
QY	541	CGCCACACAGGAGGAGTCCCTGTCGCGAGTGGATGGTGGTGAATAAGAGGCCCAT	600
DB	541	CGCCACACAGGAGGAGTCCCTGTCGCGAGTGGATGGTGGTGAATAAGAGGCCCAT	600
QY	601	GACTCTGAACAGACGAGAACATTTGACACAGGGCTGACCAATACCTGATCATCAGGCAG	660
DB	601	GACTCTGAACAGACGAGAACATTTGACACAGGGCTGACCAATACCTGATCATCAGGCAG	660
QY	661	GACGGCTCTGGACTCAGGAAATTAACCTGATGCGAGCAACATCGTGGCTTAAGAGG	720
DB	661	GACGGCTCTGGACTCAGGAAATTAACCTGATGCGAGCAACATCGTGGCTTAAGAGG	720
QY	721	AGAGCCCTGTCCGCCACTGTTGTGCTTACGTGATGGAGCTGGGAGTGTGGAGCGAA	780
DB	721	AGAGCCCTGTCCGCCACTGTTGTGCTTACGTGATGGAGCTGGGAGTGTGGAGCGAA	780

QY	781	TGGTCCGCTCTCAGTCCAGAGTGTGAACATTTTGGGATCCGGAGTGTCAGACGACCC	840
DB	781	TGGTCCGCTCTCAGTCCAGAGTGTGAACATTTTGGGATCCGGAGTGTCAGACGACCC	840
QY	841	CCGAGAAATGGGCGAAATTTCTGAGAGTCTTAAGCCAGGAATCTGAAAATCTGCACAGAT	900
DB	841	CCGAGAAATGGGCGAAATTTCTGAGAGTCTTAAGCCAGGAATCTGAAAATCTGCACAGAT	900
QY	901	GGTCTTTGCATCTAGATATAAAAAACCTCTTCATGAATAAATAACCCCAAGCATTTGAGAT	960
DB	901	GGTCTTTGCATCTAGATATAAAAAACCTCTTCATGAATAAATAACCCCAAGCATTTGAGAT	960
QY	961	GCCAGCGACATTTGCTTGTATCTGGGCTTGGGTGCTGCGCTGTCGCGCTGTCAGTCTG	1020
DB	961	GCCAGCGACATTTGCTTGTATCTGGGCTTGGGTGCTGCGCTGTCGCGCTGTCAGTCTG	1020
QY	1021	GTCAATTTGCTACCCCTTTTACAGCGGAGCGAGTGAATGCGGTGCGAGCTCAATTGAC	1080
DB	1021	GTCAATTTGCTACCCCTTTTACAGCGGAGCGAGTGAATGCGGTGCGAGCTCAATTGAC	1080
QY	1081	TCTTCTGCAATTTGACAGAGTGGCTTCCAGACCTTCAACTTTCAAAACAGTCCGTCAA	1140
DB	1081	TCTTCTGCAATTTGACAGAGTGGCTTCCAGACCTTCAACTTTCAAAACAGTCCGTCAA	1140
QY	1141	AATATCATGGAACCTAATGATACAGAAATAATCTTTGGTAACTCCCTGCTCTGAAATCT	1200
DB	1141	AATATCATGGAACCTAATGATACAGAAATAATCTTTGGTAACTCCCTGCTCTGAAATCT	1200
QY	1201	GCCATGACGAGCAGATCTGACAGTGAAGCGGACATACAGCGGACCCATCTGTCTGAGGAC	1260
DB	1201	GCCATGACGAGCAGATCTGACAGTGAAGCGGACATACAGCGGACCCATCTGTCTGAGGAC	1260
QY	1261	CCTCTGGAACAAGAGCTCATGACAGTCTTCACTCTTTAAACCTTTGTCGACATCAAA	1320
DB	1261	CCTCTGGAACAAGAGCTCATGACAGTCTTCACTCTTTAAACCTTTGTCGACATCAAA	1320
QY	1321	GTGAAAGTCCAGAGTCTGTCATGTTTCCCTGGAGTGTCTGAGAGCTGAGTACCAC	1380
DB	1321	GTGAAAGTCCAGAGTCTGTCATGTTTCCCTGGAGTGTCTGAGAGCTGAGTACCAC	1380
QY	1381	GGCAAGAAATCAATCCAGGACTTTTCCCATGGAACCAACCAAGCTTTAGTACAATGCAAT	1440
DB	1381	GGCAAGAAATCAATCCAGGACTTTTCCCATGGAACCAACCAAGCTTTAGTACAATGCAAT	1440
QY	1441	CCGAGAAATAAATGCGCTTACATCAAAATCTGTCTCATCTCCCAAGGACAGACATG	1500
DB	1441	CCGAGAAATAAATGCGCTTACATCAAAATCTGTCTCATCTCCCAAGGACAGACATG	1500
QY	1501	AGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGTG	1560
DB	1501	AGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGTG	1560
QY	1561	AGCTTACTCATACACAGCGTGCATCCAGAGGAGAAATTTGGGAGATTTATATGTC	1620
DB	1561	AGCTTACTCATACACAGCGTGCATCCAGAGGAGAAATTTGGGAGATTTATATGTC	1620
QY	1621	ATCAACCAAGAGTGAACCCAGCGCTCCAGTCAAGTGTGCTCTGAGTGTCTGAGTCTGAA	1680
DB	1621	ATCAACCAAGAGTGAACCCAGCGCTCCAGTCAAGTGTGCTCTGAGTGTCTGAGTCTGAA	1680
QY	1681	GTCACTGTGTCTCTCCAGACATGATGTCACCATCTCCCTTTGCAATTTGACCATCCCGCAC	1740
DB	1681	GTCACTGTGTCTCTCCAGACATGATGTCACCATCTCCCTTTGCAATTTGACCATCCCGCAC	1740
QY	1741	TGTGAGATGTCAATTTGAGCAATTTGGAATATCCATTTAAAGAGAGGACACAGCAGGCG	1800
DB	1741	TGTGAGATGTCAATTTGAGCAATTTGGAATATCCATTTAAAGAGAGGACACAGCAGGCG	1800
QY	1801	AAATGGAGGAGTGTGATGTCAGTGAAGATGATCTACATCTGTTTACTGCTTTTGGAC	1860
DB	1801	AAATGGAGGAGTGTGATGTCAGTGAAGATGATCTACATCTGTTTACTGCTTTTGGAC	1860
QY	1861	CCCTTTTGGCTGTCTGCTCTGAGAGCTTTGGGACCTATGCGCTCACTGAGAGGCCA	1920
DB	1861	CCCTTTTGGCTGTCTGCTCTGAGAGCTTTGGGACCTATGCGCTCACTGAGAGGCCA	1920



Db	901	 GGTCTTTGCATCCTAG-----	 -----GCAATTGAGAAT	927
Qy	961	GCACGGACGCAATTCGCTTTTACTCGGGCTTGGGTGCTGCGGTGCTGGCGTTCGAGTCCTG	1020	
Db	928	GCACGGACGCAATTCGCTTTTACTCGGGCTTGGGTGCTGCGGTGCTGGCGTTCGAGTCCTG	987	
Qy	1021	GTCAATTTGGTGTCAACCTTTTACAGACGGAGCCAGAGTGACTATGGCGGTGGACGCTCAATTGAC	1080	
Db	988	GTCAATTTGGTGTCAACCTTTTACAGACGGAGCCAGAGTGACTATGGCGGTGGAGCTCAATTGAC	1047	
Qy	1081	TCCTTCTGCATTTGACAGGTTGGCTTTCAGACCTTCACACTTCAAAACAGTCCGTCACGCCAAG	1140	
Db	1048	TCCTTCTGCATTTGACAGGTTGGCTTTCAGACCTTCACACTTCAAAACAGTCCGTCACAA	1101	
Qy	1141	AATATCATGGAACTAATGATACAAGAAAAATCTTTTGGTAACTCCCTGCTCCTGAAATTC	1200	
Db	1102	-----GGTAACTCCCTGCTCCTGAAATTC	1125	
Qy	1201	GCCATCAGCCAGATCTGACAGTGACCGGACATACAGCGGACCCATCTGTCTGCAGGAC	1260	
Db	1126	GCCATCAGCCAGATCTGACAGTGACCGGACATACAGCGGACCCATCTGTCTGCAGGAC	1185	
Qy	1261	CCTCTGGACAAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTTTCGACATCAAA	1320	
Db	1186	CCTCTGGACAAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTTTCGACATCAAA	1245	
Qy	1321	GTGAAAGTCAGAGCTCGTTTCATGGTTTCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC	1380	
Db	1246	GTGAAAGTCAGAGCTCGTTTCATGGTTTCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC	1305	
Qy	1381	GGCAAGATCATTTCCAGGACTTTTCCCATGGGAACAACACACAGCTTTAGTCAATGCAT	1440	
Db	1306	GGCAAGATCATTTCCAGGACTTTTCCCATGGGAACAACACACAGCTTTAGTCAATGCAT	1365	
Qy	1441	CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCACTATCCCAACAGGACAGAACTG	1500	
Db	1366	CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCACTATCCCAACAGGACAGAACTG	1425	
Qy	1501	AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGGCTTAGTAATGCCAATACAGGGTG	1560	
Db	1426	AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGGCTTAGTAATGCCAATACAGGGTG	1485	
Qy	1561	AGCTTACTCATACACACGGTGGCCATCCACAGAGAGAAATTCCTTTGGGAGATTTATATGTC	1620	
Db	1486	AGCTTACTCATACACACGGTGGCCATCCACAGAGAGAAATTCCTTTGGGAGATTTATATGTC	1545	
Qy	1621	ATCAACCAAGGTGAACCCAGGCTCCAGTCAGATGGCTCTGAGTGTCTCTGAGTCTCTGAA	1680	
Db	1546	ATCAACCAAGGTGAACCCAGGCTCCAGTCAGATGGCTCTGAGTGTCTCTGAGTCTCTGAA	1605	
Qy	1681	GTCACTTGTGTCTCTCAGACATGATCGTCAACACTCCCTTTGCAATTCAGCCATCCCGCAC	1740	
Db	1606	GTCACTTGTGTCTCTCAGACATGATCGTCAACACTCCCTTTGCAATTCAGCCATCCCGCAC	1665	
Qy	1741	TGTGCAGATGTCAGTTCTGAGCATTTGGAATATCCATTTAAAGAAAGGACACACAGCAGGC	1800	
Db	1666	TGTGCAGATGTCAGTTCTGAGCATTTGGAATATCCATTTAAAGAAAGGACACACAGCAGGC	1725	
Qy	1801	AAATGGGAGGAAGTGATGTCACTAGTGGAAATGAAATCACTCCCTGTCTACTGCTTTTGGAC	1860	
Db	1726	AAATGGGAGGAAGTGATGTCACTAGTGGAAATGAAATCACTCCCTGTCTACTGCTTTTGGAC	1785	
Qy	1861	CCCTTTGCGTGTCAATGTCTCCTCGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA	1920	
Db	1786	CCCTTTGCGTGTCAATGTCTCCTCGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA	1845	
Qy	1921	ATCAGACAGCTGCGGTGAAGCAACTGAAGTGGCGTTTTTGGTCTCATGTCTCTGTAA	1980	
Db	1846	ATCAGACAGCTGCGGTGAAGCAACTGAAGTGGCGTTTTTGGTCTCATGTCTCTGTAA	1905	
Qy	1981	TCCCTGGATTACAACTTCAGAGTTTATCTGTGTGGACAAATACCCCTTGTGCAATTCAGAA	2040	

1906	TCCTCGGATTCAACCTTGAGAGTTTACTGTGTGGACAATACCCCTGTGCACTTTCAGGAA	1961
2041	GTGGTTTCAGATGAAGAGGCATCAAGGTGACAGCTCCTCGAAGAACCAAAAATTCGTGCAAT	2100
1966	GTGGTTTCAGATGAAGAGGCATCAAGGTGACAGCTCCTCGAAGAACCAAAAATTCGTGCAAT	2025
2101	TTCAAAAGGGAATACCTTTAGTCTTTCAGATTTCTGTGTCCTTGATATTCGCCCATTCCTCTG	2160
2026	TTCAAAAGGGAATACCTTTAGTCTTTCAGATTTCTGTGTCCTTGATATTCGCCCATTCCTCTG	2085
2161	AGAAATTAACCAATTCACCTGCTGCCAGGAAGTCCCGTCTTCCTCGGTGTGGTCCAGTAAC	2220
2086	AGAAATTAACCAATTCACCTGCTGCCAGGAAGTCCCGTCTTCCTCGGTGTGGTCCAGTAAC	2145
2221	CGGAGGCCCTGCATCTGTGCTTCTCGCTGGAGCGTTATACGCCCACTACCCACCCAGCTG	2280
2146	CGGAGGCCCTGCATCTGTGCTTCTCGCTGGAGCGTTATACGCCCACTACCCACCCAGCTG	2205
2281	TCCTGCAAAATCTGCATTTCCGCGAGCTCAAAAGGCCATGAACAGATCTCTCAAGTGCAGACA	2340
2206	TCCTGCAAAATCTGCATTTCCGCGAGCTCAAAAGGCCATGAACAGATCTCTCAAGTGCAGACA	2265
2341	TCAATCTCAGAGAGTGAAAGAGAAAACAATCATTTCTTTCGCCACAAGAGGACAGCACTTTC	2400
2266	TCAATCTCAGAGAGTGAAAGAGAAAACAATCATTTCTTTCGCCACAAGAGGACAGCACTTTC	2325
2401	CCTGCAAGACTGGCCCCCAAGCCTTCAAAATTTCCCTACTCCATTCAGACAGCGGATTTGT	2460
2326	CCTGCAAGACTGGCCCCCAAGCCTTCAAAATTTCCCTACTCCATTCAGACAGCGGATTTGT	2385
2461	GCTACATTTGATACCCCCAATGCCAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAC	2520
2386	GCTACATTTGATACCCCCAATGCCAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAC	2445
2521	AGCATCAACAGGAATTTATCTTATTTTCGCTACACAAGAGTAGCCCATCTGCTGTCATTTTG	2580
2446	AGCATCAACAGGAATTTATCTTATTTTCGCTACACAAGAGTAGCCCATCTGCTGTCATTTTG	2505
2581	AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGGCCTT	2640
2506	AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGGCCTT	2565
2641	GAAAGATTGGGAGGACACACAGAAACTCTCAAACTTTTCAGAAATCCACAGCTTGATGAA	2700
2566	GAAAGATTGGGAGGACACACAGAAACTCTCAAACTTTTCAGAAATCCACAGCTTGATGAA	2625
2701	GCCGACTTCAACTACAGCAGGCAAAAATGGACTCTAG	2736
2626	GCCTACTTCACTACAGCAGCAAAAATGGACTCTAG	2661

RESULT 6  
US-09-969-532-25  
; Sequence 25, Application US/09969532  
; Patent No. 6777232

```

: GENERAL INFORMATION:
: APPLICANT: Walke, D. Wade
: APPLICANT: Scoville, John
: TITLE OF INVENTION: No. 6772732e1 Human Membrane Proteins and Polynucleotides Encodu
: FILE REFERENCES: LEX-0244-USA
: CURRENT APPLICATION NUMBER: US/09/969,532
: CURRENT FILING DATE: 2001-10-02
: PRIOR APPLICATION NUMBER: US 60/237,280
: PRIOR FILING DATE: 2000-10-02
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 25
: LENGTH: 2043
: TYPE: DNA
: ORGANISM: homo sapiens
: US-09-969-532-25

```

Query Match 74.7%; Score 2043; DB 4; Length 2043;

Best Local Similarity 100.0%; Pred. No. 0; Matches 2043; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	694	ATGCGACCCAAACATCTGTGGCTTAAGAGGAGAACCTGTGGCCCACTGTGTGGTCTACGTG	753	
Db	1	ATGCGACCCAAACATCTGTGGCTTAAGAGGAGAACCTGTGGCCCACTGTGTGGTCTACGTG	60	
Qy	754	GATGGGAGCTGGGAAGTGTGGAGCGGAATGTGCGTCTGCGATGCGAGTGTGAACATTTG	813	
Db	61	GATGGGAGCTGGGAAGTGTGGAGCGGAATGTGCGTCTGCGATGCGAGTGTGAACATTTG	120	
Qy	814	CGGATCCGGAGTGCACAGCACCAACCCCGAGAAATGGGGGCAAAATCTGTGAAGGCTA	873	
Db	121	CGGATCCGGAGTGCACAGCACCAACCCCGAGAAATGGGGGCAAAATCTGTGAAGGCTA	180	
Qy	874	AGCCAGGAATCTGAAATCTGCACAGATGGTCTTTGCACTCTAGATAAAAAACCTCTTCAT	933	
Db	181	AGCCAGGAATCTGAAATCTGCACAGATGGTCTTTGCACTCTAGATAAAAAACCTCTTCAT	240	
Qy	934	GAATAAACCACCAAGCATTGAGATGCGAGAGCAATGCTTTGTACTCGGGCTTGGGT	993	
Db	241	GAATAAACCACCAAGCATTGAGATGCGAGAGCAATGCTTTGTACTCGGGCTTGGGT	300	
Qy	994	GCTGCCGTGCTGGCGTTGCAGTCTGCTCATTTGCTCACTTACAGACGAGCCAG	1053	
Db	301	GCTGCCGTGCTGGCGTTGCAGTCTGCTCATTTGCTCACTTACAGACGAGCCAG	360	
Qy	1054	AGTGACTATGGCGTGGAGCTCAATTGACTCTTCTGCAATGAGAGTGGCTTCCAGACCTTC	1113	
Db	361	AGTGACTATGGCGTGGAGCTCAATTGACTCTTCTGCAATGAGAGTGGCTTCCAGACCTTC	420	
Qy	1114	AATTTCAAAACAGTCTCGTCAAGCAAGAAATATCATGGAATTAATGATPACAAGAAAATCC	1173	
Db	421	AATTTCAAAACAGTCTCGTCAAGCAAGAAATATCATGGAATTAATGATPACAAGAAAATCC	480	
Qy	1174	TTTGGTAACTCCCTGCTCCCTGAATTTCTGCCATGCGAGCCAGATCTGACAGTGAGCCGGACA	1233	
Db	481	TTTGGTAACTCCCTGCTCCCTGAATTTCTGCCATGCGAGCCAGATCTGACAGTGAGCCGGACA	540	
Qy	1234	TACAGCGGACCCCATCTGTCTGCGAGGACCTCTGGACAAAGGAGCTCATGACAGAGTCTCTCA	1293	
Db	541	TACAGCGGACCCCATCTGTCTGCGAGGACCTCTGGACAAAGGAGCTCATGACAGAGTCTCTCA	600	
Qy	1294	CTCTTTAACCCCTTTGTGCGGACATCAAAAGTGAAGTCCAGAGTCTGTTTCCTTG	1353	
Db	601	CTCTTTAACCCCTTTGTGCGGACATCAAAAGTGAAGTCCAGAGTCTGTTTCCTTG	660	
Qy	1354	GGAGTGTCTGAGAGCTGAGTACCAAGCAAGAAATCAATTTCCAGGACTTTTCCCATGGA	1413	
Db	661	GGAGTGTCTGAGAGCTGAGTACCAAGCAAGAAATCAATTTCCAGGACTTTTCCCATGGA	720	
Qy	1414	AACAACCAAGCTTTTGTAGTACAAATGCATCCAGAAATAAATGCCCTACATCCAAAATCTG	1473	
Db	721	AACAACCAAGCTTTTGTAGTACAAATGCATCCAGAAATAAATGCCCTACATCCAAAATCTG	780	
Qy	1474	TCATCACTCCCAAGGACAGAACTGAGCAAACTGGTGTCTTTGGCCATTTAGGGGGG	1533	
Db	781	TCATCACTCCCAAGGACAGAACTGAGCAAACTGGTGTCTTTGGCCATTTAGGGGGG	840	
Qy	1534	CGCTTAGTAATGCCAATAACGGGGTGAATCTTACTATACACAGGTGCGATCCAGAG	1593	
Db	841	CGCTTAGTAATGCCAATAACGGGGTGAATCTTACTATACACAGGTGCGATCCAGAG	900	
Qy	1594	GAGAAATCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCTTCCAGTCAAT	1653	
Db	901	GAGAAATCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCTTCCAGTCAAT	960	
Qy	1654	GGCTCTGAGTGTCTCTGAGTCTCTGAAAGTCACTGTGGTCTCTCCAGACATGATCGTCAAC	1713	
Db	961	GGCTCTGAGTGTCTCTGAGTCTCTGAAAGTCACTGTGGTCTCTCCAGACATGATCGTCAAC	1020	
Qy	1714	ACTCCCTTTGCAATGACCATCCCGCACTGTGCGAGTGTGAGTCTGAGCAATTTGAATATC	1773	

RESULT 7  
US-09-969-532-27

Db	1021	ACTCCCTTTGCATTGACCATCCCGCACTGTGCGATGTGAGTCTGAGCAATTTGAATATC	1080	
Qy	1774	CATTTAAAGAGAGGACACACAGAGGCAAAATGGAGGAAGTGTGATGTCAGTGGGAAGATGAA	1833	
Db	1081	CATTTAAAGAGAGGACACACAGAGGCAAAATGGAGGAAGTGTGATGTCAGTGGGAAGATGAA	1140	
Qy	1834	TCTACATCTCTGTTACTGCTTTTGGACCCCTTTTGGACCCCTTTCGCTGTCTATGCTCTCTGGACAGCTTT	1893	
Db	1141	TCTACATCTCTGTTACTGCTTTTGGACCCCTTTTGGACCCCTTTCGCTGTCTATGCTCTCTGGACAGCTTT	1200	
Qy	1894	GGGACCTATGCGCTCACTGAGAGCCAAATCAACAGACTGTGCGGTGAAGCAACTGAAGGTG	1953	
Db	1201	GGGACCTATGCGCTCACTGAGAGCCAAATCAACAGACTGTGCGGTGAAGCAACTGAAGGTG	1260	
Qy	1954	GCGGTTTTGGCTGCGATGCTGTAACTCCCTCGAATTAACCTTGAGAGTTTACTGTGTG	2013	
Db	1261	GCGGTTTTGGCTGCGATGCTGTAACTCCCTCGAATTAACCTTGAGAGTTTACTGTGTG	1320	
Qy	2014	GACAATACCCCTTGTGCNTTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG	2073	
Db	1321	GACAATACCCCTTGTGCNTTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG	1380	
Qy	2074	CTCTCTGGAAGAACCAAAATTTGCTGCAATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT	2133	
Db	1381	CTCTCTGGAAGAACCAAAATTTGCTGCAATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT	1440	
Qy	2134	GTCTTTGATATTTCCCTTCTCTGAGAAATTAACCAATTTCACTGCTGCCAGGAATGTC	2193	
Db	1441	GTCTTTGATATTTCCCTTCTCTGAGAAATTAACCAATTTCACTGCTGCCAGGAATGTC	1500	
Qy	2194	CGGTTCTCCGCGTGTGGTGCAGTAACCGGACGCCCTGCACTGTGCTTCTCCCTGGAG	2253	
Db	1501	CGGTTCTCCGCGTGTGGTGCAGTAACCGGACGCCCTGCACTGTGCTTCTCCCTGGAG	1560	
Qy	2254	CGTTATAGGCCACTACCAACCCAGCTGTCTGCAAAATCTGCAATTCGGCAGCTCAAAAGGC	2313	
Db	1561	CGTTATAGGCCACTACCAACCCAGCTGTCTGCAAAATCTGCAATTCGGCAGCTCAAAAGGC	1620	
Qy	2314	CATGAAACAGATCTTCAAGTGCAGACATCAATCTTAGAGAGTGAAGAGAAACCATCACT	2373	
Db	1621	CATGAAACAGATCTTCAAGTGCAGACATCAATCTTAGAGAGTGAAGAGAAACCATCACT	1680	
Qy	2374	TTCTTTCGCAAGAGGACAGACATTTTCCCTGCAAGACTGCGCCCAAGGCTTCAAAATTT	2433	
Db	1681	TTCTTTCGCAAGAGGACAGACATTTTCCCTGCAAGACTGCGCCCAAGGCTTCAAAATTT	1740	
Qy	2434	CCCTACTCTCATCAGACAGCGGATTTGTGCTTACATTTTGATACCCCAATGCAAGGCAAG	2493	
Db	1741	CCCTACTCTCATCAGACAGCGGATTTGTGCTTACATTTTGATACCCCAATGCAAGGCAAG	1800	
Qy	2494	GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTTCGTACAC	2553	
Db	1801	GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTTCGTACAC	1860	
Qy	2554	CAAAAGTAGCCCATCTGCTGTCAATTTGAACTGTGGGAAGCTCGTCACTAGCATGATGGT	2613	
Db	1861	CAAAAGTAGCCCATCTGCTGTCAATTTGAACTGTGGGAAGCTCGTCACTAGCATGATGGT	1920	
Qy	2614	GATCTTGACTCTCCCTGCGCTGTGCCCTTGAAGAGATTTGGGAGGACACACACGAAACTCTCA	2673	
Db	1921	GATCTTGACTCTCCCTGCGCTGTGCCCTTGAAGAGATTTGGGAGGACACACACGAAACTCTCA	1980	
Qy	2674	AACATTTTCAAGATCCAGCTTTGATGAAGCGGACTTCAACTACAGAGGCAAAATGGATCTC	2733	
Db	1981	AACATTTTCAAGATCCAGCTTTGATGAAGCGGACTTCAACTACAGAGGCAAAATGGATCTC	2040	
Qy	2734	TAG 2736		
Db	2041	TAG 2043		













		Matches 1607; Conservative 0; Mismatches 0; Indels 33; Gaps 1;	
Qy	961	GCACAGCAATTCCTTTGTAATCGGCTTGGGTGCTGCGCTGTCGCGCTTGCAGTCTCTG	1020
Db	961	GCACAGCAATTCCTTTGTAATCGGCTTGGGTGCTGCGCTGTCGCGCTTGCAGTCTCTG	1020
Qy	1021	GTCAATGGGTGTCACCTTTTACAGAGGAGCCAGAGTGAATATGGCGTGACAGTCAATTGAC	1080
Db	1021	GTCAATGGGTGTCACCTTTTACAGAGGAGCCAGAGTGAATATGGCGTGACAGTCAATTGAC	1080
Qy	1081	TCCTTCTGCAATGACAGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG	1140
Db	1081	TCCTTCTGCAATGACAGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG	1140
Qy	1141	AATATCATGAACATAATGATAAAGAAATCTTTGGTAACTCCCTGCTCTGTAATCT	1200
Db	1141	AATATCATGAACATAATGATAAAGAAATCTTTGGTAACTCCCTGCTCTGTAATCT	1200
Qy	1201	GCCATGAGCCAGATCTGACAGTGGAGCCGACATACAGGGGACCCATCTGTCTGCAGGAC	1260
Db	1201	GCCATGAGCCAGATCTGACAGTGGAGCCGACATACAGGGGACCCATCTGTCTGCAGGAC	1260
Qy	1261	CCTCTGGACAAGAGTCTCATGACAGAGTCTCACTCTTTAAACCTTTTGTGGACATCAAA	1320
Db	1261	CCTCTGGACAAGAGTCTCATGACAGAGTCTCACTCTTTAAACCTTTTGTGGACATCAAA	1320
Qy	1321	GTGAAGTCCAGAGTCTGTTCATGCTTCCCTGGAGTGTCTGAGAGCTGAGTACCAC	1380
Db	1321	GTGAAGTCCAGAGTCTGTTCATGCTTCCCTGGAGTGTCTGAGAGCTGAGTACCAC	1380
Qy	1381	GGCAAGATCATTTCCAGGACTTTTCCCATGGAACAAACACAGCTTTTGTAGTCAATGCAT	1440
Db	1381	GGCAAGATCATTTCCAGGACTTTTCCCATGGAACAAACACAGCTTTTGTAGTCAATGCAT	1440
Qy	1441	CCCAGAAATAAATGCCCTCATCATCCAAATCTGTCTATCATCTCCCAAGGACAGAACTG	1500
Db	1441	CCCAGAAATAAATGCCCTCATCATCCAAATCTGTCTATCATCTCCCAAGGACAGAACTG	1500
Qy	1501	AGGACAACTGGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG	1560
Db	1501	AGGACAACTGGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG	1560
Qy	1561	AGCTTACTATACACACAGTGGCCATCCAGAGGAGAAATCTTTGGGAGATTTATATGTC	1620
Db	1561	AGCTTACTATACACACAGTGGCCATCCAGAGGAGAAATCTTTGGGAGATTTATATGTC	1620
Qy	1621	ATCAACCAAGTGAACCCAG 1640	
Db	1621	ATCAACCAAGTGAACCCAG 1640	
RESULT 11			
US-969-532-3			
; Sequence 3, Application US/09969532			
; Patent No. 6777232			
; GENERAL INFORMATION:			
; APPLICANT: Walke, D. Wade			
; APPLICANT: Scoville, John			
; TITLE OF INVENTION: No. 677232a1 Human Membrane Proteins and Polynucleotides Encodin			
; FILE REFERENCE: LEX-0244-USA			
; CURRENT APPLICATION NUMBER: US/09/969,532			
; CURRENT FILING DATE: 2001-10-02			
; PRIOR APPLICATION NUMBER: US 60/237,280			
; PRIOR FILING DATE: 2000-10-02			
; NUMBER OF SEQ ID NOS: 33			
; SOFTWARE: FASTSEQ for Windows Version 4.0			
; SEQ ID NO 3			
; LENGTH: 1701			
; TYPE: DNA			
; ORGANISM: homo sapiens			
US-09-969-532-3			
Query Match 57.2%; Score 1564; DB 4; Length 1701;			
Best Local Similarity 98.0%; Pred. No. 0;			

QY 1081 TCTTCTGATTTGACAGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAA 1140  
DB 1048 TCTTCTGATTTGACAGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAA 1107  
QY 1141 AATATCATGGAATCAATGATACAGAAATCCCTTTGGTAACTCCCTGCTCTCTGAAATCT 1200  
DB 1108 AATATCATGGAATCAATGATACAGAAATCCCTTTGGTAACTCCCTGCTCTCTGAAATCT 1167  
QY 1201 GCCATGAGCCAGATCTGACAGTGGAGCCGACATACAGCGGACCCATCTGTCTGCAGGAC 1260  
DB 1168 GCCATGAGCCAGATCTGACAGTGGAGCCGACATACAGCGGACCCATCTGTCTGCAGGAC 1227  
QY 1261 CCTCTGACAGGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTTGTGCGACATCAA 1320  
DB 1228 CCTCTGACAGGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTTGTGCGACATCAA 1287  
QY 1321 GTGAAAGTCCAGAGCTGTTTCATGTTTCCCTGGGAGTGTCTGAGAGAGTGTGAGTACCAC 1380  
DB 1288 GTGAAAGTCCAGAGCTGTTTCATGTTTCCCTGGGAGTGTCTGAGAGAGTGTGAGTACCAC 1347  
QY 1381 GGCAAGAAATCAATCCAGGACTTTTCCCATGGAACCAACACAGCTTTTAGTACAATGCAT 1440  
DB 1348 GGCAAGAAATCAATCCAGGACTTTTCCCATGGAACCAACACAGCTTTTAGTACAATGCAT 1407  
QY 1441 CCCAGAAATAAATGCCCTACATCCAAATCTGTCTCATCTCCCAACAGGACAGAACTG 1500  
DB 1408 CCCAGAAATAAATGCCCTACATCCAAATCTGTCTCATCTCCCAACAGGACAGAACTG 1467  
QY 1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGGCTTAGTAAATGCCAAATACAGGGGTG 1560  
DB 1468 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGGCTTAGTAAATGCCAAATACAGGGGTG 1527  
QY 1561 AGCTTACTCATACACACAGTGGCCATCCAGAGGAGAAATCTTGGGAGATTTATATGTCC 1620  
DB 1528 AGCTTACTCATACACACAGTGGCCATCCAGAGGAGAAATCTTGGGAGATTTATATGTCC 1587  
QY 1621 ATCAACCAAGTGAACCCAG 1640  
DB 1588 ATCAACCAAGTGAACCCAG 1607

## RESULT 12

US-09-969-532-5  
; Sequence 5, Application US/09969532  
; Patent No. 677232  
; GENERAL INFORMATION:  
; APPLICANT: Walke, D. Wade  
; APPLICANT: Scoville, John  
; TITLE OF INVENTION: No. 677232zel Human Membrane Proteins and Polynucleotides Encodin  
; FILE REFERENCE: LEX-0244-USA  
; CURRENT APPLICATION NUMBER: US/09/969,532  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 60/237,280  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1692  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-969-532-5

Query Match 56.5%; Score 1546; DB 4; Length 1692;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1598; Conservative 0; Mismatches 0; Indels 42; Gaps 1;  
QY 1 ATGGGAGAGCGGCGCCACCGCAGCGGCGGCGGAGCGGCGCGCTGGCTCCCGTGG 60  
DB 1 ATGGGAGAGCGGCGCCACCGCAGCGGCGGCGGAGCGGCGCGCTGGCTCCCGTGG 60  
QY 61 CTGGGCTGTCTTGGGGCGGAGGACCGCGGCTGCCGAGGAACTGACATGGGAA 120

DB 61 CTGGGCTGTCTTGGGCGGAGGACCGCGGCTGCCGAGGAACTGACATGGGAA 120  
QY 121 GCCCTTCCGAAATCCATCCCATGCTCTGGGACACTGCTCTCATTTTCATAGAGAGCCA 180  
DB 121 GCCCTTCCGAAATCCATCCCATGCTCTGGGACACTGCTCTCATTTTCATAGAGAGCCA 180  
QY 181 GATGATGCTTATATATCAAGAGCACCCTATTGCACTCAGGTGCAAGCGGAGGCCGCC 240  
DB 181 GATGATGCTTATATATCAAGAGCACCCTATTGCACTCAGGTGCAAGCGGAGGCCGCC 240  
QY 241 ATGCAGATATTTCTTCAAAATGCAACGGGAGTGGGTCCATCAGAACAGGACGCTCTCTGAA 300  
DB 241 ATGCAGATATTTCTTCAAAATGCAACGGGAGTGGGTCCATCAGAACAGGACGCTCTCTGAA 300  
QY 301 GAGACTCTGACAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTTACTAGG 360  
DB 301 GAGACTCTGACAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTTACTAGG 360  
QY 361 CAACAGGTGGAGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420  
DB 361 CAACAGGTGGAGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420  
QY 421 CACTGGGTACCTTCCAAAGAGCAGAGGCTCTGTGGGCATAGCTTATTTACGGAATAAC 480  
DB 421 CACTGGGTACCTTCCAAAGAGCAGAGGCTCTGTGGGCATAGCTTATTTACGGAATAAC 480  
QY 481 TTTTGAACAAGACCCCAAGGAAGGAAAGTTCCCATTTGAAGGCATGATTTGACTGCACTGC 540  
DB 481 TTTTGAACAAGACCCCAAGGAAGGAAAGTTCCCATTTGAAGGCATGATTTGACTGCACTGC 540  
QY 541 CGGCCACAGAGAGGAGTCCCTGCTGCGGAGTGGAAATGGCTGAAAAATGAAGAGCCCAT 600  
DB 541 CGGCCACAGAGAGGAGTCCCTGCTGCGGAGTGGAAATGGCTGAAAAATGAAGAGCCCAT 600  
QY 601 GACTCTGAAACAAGACAGAAACATTTGACACAGGCTGACCATTAACCTGATCATCAGGAG 660  
DB 601 GACTCTGAAACAAGACAGAAACATTTGACACAGGCTGACCATTAACCTGATCATCAGGAG 660  
QY 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGATGCGAGCAACATCGTGGCTAAGAGG 720  
DB 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGATGCGAGCAACATCGTGGCTAAGAGG 720  
QY 721 AGAAGCTCTCGGCCACTGTTGGTCTACGTGGATGGGAGCTGGGAAAGTGTGGAGCGAA 780  
DB 721 AGAAGCTCTCGGCCACTGTTGGTCTACGTGGATGGGAGCTGGGAAAGTGTGGAGCGAA 780  
QY 781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTTCGGATCCGGAGTGCACAGCACACCCC 840  
DB 781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTTCGGATCCGGAGTGCACAGCACACCCC 840  
QY 841 CCGAGAAATGGGGGCAAAATTTCTGTGAAGTCTTAAGCCAGGAATCTGAAAACTGCACAGAT 900  
DB 841 CCGAGAAATGGGGGCAAAATTTCTGTGAAGTCTTAAGCCAGGAATCTGAAAACTGCACAGAT 900  
QY 901 GGTCTTTGCAATCTAGATAAAAAACCTTCTCATGAAATAAAAAACCCAAAGCATTTGAGAAT 960  
DB 901 GGTCTTTGCAATCTAGATAAAAAACCTTCTCATGAAATAAAAAACCCAAAGCATTTGAGAAT 960  
QY 961 GCCAGCGACATCTCTTGTACTCGGGCTTGGGTGCTGCGCTGCTGGCGCTTGCAGTCTTG 1020  
DB 961 GCCAGCGACATCTCTTGTACTCGGGCTTGGGTGCTGCGCTGCTGGCGCTTGCAGTCTTG 1020  
QY 1021 GTCAATGGGTGTCACCCCTTTACAGACGAGGACGAGAGTACTATGGCGTGGAGCTCATTTGAC 1080  
DB 1021 GTCAATGGGTGTCACCCCTTTTACAGACGAGGACGAGAGTACTATGGCGTGGAGCTCATTTGAC 1080  
QY 1081 TCTTCTGCAATTTGACAGTGGCTTCCAGACCTTCAACTTTCAAAAACAGTCCGTCAGGCCAAG 1140  
DB 1081 TCTTCTGCAATTTGACAGTGGCTTCCAGACCTTCAACTTTCAAAAACAGTCCGTCAGGCCAAG 1134  
QY 1141 AATATCATGGAATCAATGATACAGAAATCTTTGGTAACTCCCTGCTCTGAAATTTCT 1200  
DB 1135 -----GGTAACTCCCTGCTCTGAAATTTCT 1158

```

QY 1201 GCCATGAGCCAGATCTGACAGTACGCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
Db 1159 GCCATGAGCCAGATCTGACAGTACGCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1218
QY 1261 CCTCTGGACNAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTGTGCGACATCAA 1320
Db 1219 CCTCTGGACNAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTGTGCGACATCAA 1278
QY 1321 GTCAAAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTGTCTGAGAGCTGAGTACCA 1380
Db 1279 GTCAAAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTGTCTGAGAGCTGAGTACCA 1338
QY 1381 GGCAAGATCAATTCAGGACTTTTCCCATGGAACCAACACAGCTTTTGTAGTCAATGCAT 1440
Db 1339 GGCAAGATCAATTCAGGACTTTTCCCATGGAACCAACACAGCTTTTGTAGTCAATGCAT 1398
QY 1441 CCCAGAAATAAATGCCCTACATCCAAATCTCTCATCACTCCCAACAGGACAGAACTG 1500
Db 1399 CCCAGAAATAAATGCCCTACATCCAAATCTCTCATCACTCCCAACAGGACAGAACTG 1458
QY 1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCAAAATACAGGGTG 1560
Db 1459 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCAAAATACAGGGTG 1518
QY 1561 AGCTTACTATACACAGGTGCTCCATCCAGAGGAGAAATCTTGGGAGATTTATATGTC 1620
Db 1519 AGCTTACTATACACAGGTGCTCCATCCAGAGGAGAAATCTTGGGAGATTTATATGTC 1578
QY 1621 ATCAACCAAGTGAACCCAG 1640
Db 1579 ATCAACCAAGTGAACCCAG 1598

RESULT 13
US-09-969-532-7
; Sequence 7, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-7

Query Match 53.7%; Score 1470; DB 4; Length 1659;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 75; Gaps 2;

QY 1 ATGGGGAGAGCGGGCGCCACCGCAGGCGGGCGGGGCGGGCGCGCTGGCTCCCGTGG 60
Db 1 ATGGGGAGAGCGGGCGCCACCGCAGGCGGGCGGGGCGGGCGCGCTGGCTCCCGTGG 60
QY 61 CTGGGGCTGTCTTCTGGGCGGAGGACCGCGGCTGCCAGGAATGACAATGGCGAA 120
Db 61 CTGGGGCTGTCTTCTGGGCGGAGGACCGCGGCTGCCAGGAATGACAATGGCGAA 120
QY 121 GCCCTTCCCGAATCCATCCCATCAGCTCTGGGACACTGCTCAATTCATGAGAGGCCA 180
Db 121 GCCCTTCCCGAATCCATCCCATCAGCTCTGGGACACTGCTCAATTCATGAGAGGCCA 180
QY 181 GATGATGCTTATATATCAAGAGCAACCTTATGCACTCAGGTGCAAGCGGACGCGCCAGCC 240
Db 181 GATGATGCTTATATATCAAGAGCAACCTTATGCACTCAGGTGCAAGCGGACGCGCCAGCC 240
```

```

Db 181 GATGATGCTTATATATCAAGAGCAACCTTATGCACTCAGGTGCAAGCGGACGCGCCAGCC 240
QY 241 ATGACAGATATTTCTTCAATGCAACGCGAGTGGGTCCATCAGAACGAGCAGCTCTCTGAA 300
Db 241 ATGACAGATATTTCTTCAATGCAACGCGAGTGGGTCCATCAGAACGAGCAGCTCTCTGAA 300
QY 301 GAGACTCTGGACGAGAGCTCAGAGTTTGAAGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
Db 301 GAGACTCTGGACGAGAGCTCAGAGTTTGAAGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
QY 361 CAACAGTGGAGGACTTCCATGGGCGCGAGACTATTTGGTCCAGTGTGTGGCGTGGAGC 420
Db 361 CAACAGTGGAGGACTTCCATGGGCGCGAGACTATTTGGTCCAGTGTGTGGCGTGGAGC 420
QY 421 CACCTGGGTACTCTCAAGAGCAGGAAGSCCTCTGTGCGCATAGCTTATTTACGGAAAAAC 480
Db 421 CACCTGGGTACTCTCAAGAGCAGGAAGSCCTCTGTGCGCATAGCTTATTTACGGAAAAAC 480
QY 481 TTTGAACAAGACCCCAAGAGGGAAGTTCCTTGAAGGCGATGTTGTAAGGCGATGTTGTAAGGCG 540
Db 481 TTTGAACAAGACCCCAAGAGGGAAGTTCCTTGAAGGCGATGTTGTAAGGCGATGTTGTAAGGCG 540
QY 541 CGCCCAACAGAGGAGTCCCTGCTGCCAGGTGGATGGCTGMAAAATGAAGAGCCCAT 600
Db 541 CGCCCAACAGAGGAGTCCCTGCTGCCAGGTGGATGGCTGMAAAATGAAGAGCCCAT 600
QY 601 GACTCTGAACAAGACGAGAACATTTGACACACAGGGCTGACCATTAACCTGATCATCAGGCG 660
Db 601 GACTCTGAACAAGACGAGAACATTTGACACACAGGGCTGACCATTAACCTGATCATCAGGCG 660
QY 661 GCAAGCTCTCGGACCTCAGGAAATTTACCTGTCATGGCAGGCCAACATCGTGGCTAAGAGG 720
Db 661 GCAAGCTCTCGGACCTCAGGAAATTTACCTGTCATGGCAGGCCAACATCGTGGCTAAGAGG 720
QY 721 AGAAGCTCTCGGCGCCACTGTTGTGCTCTACGTGGATGGAGCTGGGAGTGTGGAGCGAA 780
Db 721 AGAAGCTCTCGGCGCCACTGTTGTGCTCTACGTGGATGGAGCTGGGAGTGTGGAGCGAA 780
QY 781 TGGTCCGCTCGCAGTCCAGAGTGTGAAATTTGCGGATCCGCGGATCCGCGGATCCGCGGATCCGCGG 840
Db 781 TGGTCCGCTCGCAGTCCAGAGTGTGAAATTTGCGGATCCGCGGATCCGCGGATCCGCGGATCCGCGG 840
QY 841 CCGAGAAATGGGGGCAAAATTTCTGCAAGTCTTAAGCCAGGATCTGAAAACCTGCACAGAT 900
Db 841 CCGAGAAATGGGGGCAAAATTTCTGCAAGTCTTAAGCCAGGATCTGAAAACCTGCACAGAT 900
QY 901 GGTCTTTGTCATCTAGATAAAAAA CCTCTTCTTCAATAAAAAACCCCAAGCAATTGAGAT 960
Db 901 GGTCTTTGTCATCTAGATAAAAAA CCTCTTCTTCAATAAAAAACCCCAAGCAATTGAGAT 960
QY 961 GCGAGCGCAATTTGCTTTGCTCTCGGGCTTTGGGTGCTGCGCTGCTGGCGGCTTGCAGTCTTG 1020
Db 961 GCGAGCGCAATTTGCTTTGCTCTCGGGCTTTGGGTGCTGCGCTGCTGGCGGCTTGCAGTCTTG 1020
QY 1021 GTCAATTTGCTCACCTTTTACAGACGAGCCAGAGTACTATGCGCTGGACGCTCATTTGAC 1080
Db 988 GTCAATTTGCTCACCTTTTACAGACGAGCCAGAGTACTATGCGCTGGACGCTCATTTGAC 1047
QY 1081 TCTTCTGCAATTTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAGCAAGCAAG 1140
Db 1048 TCTTCTGCAATTTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAGCAAGCAAG 1101
QY 1141 AATATCATGGAATTAATGATACAGAAAAATCCTTTTGTAACTCCCTGCTCTCTGAAATCT 1200
Db 1102 -----GGTAACTCCCTGCTCTCTGAAATCT 1125
QY 1201 GCCATGAGCCAGATCTGACAGTACGCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
Db 1126 GCCATGAGCCAGATCTGACAGTACGCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1185
QY 1261 CCTCTGGACNAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTGTGCGACATCAA 1320
Db 1186 CCTCTGGACNAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTGTGCGACATCAA 1245
```





61	Db	 GATGGAGCTGGGAAGTGTGGAGCGAATGGTCCGCTGCAGTCCAGAGTGTGAACATTGG	120
814	Qy	CGGATCCGGAGTGCACAGCACCACCCTGGAGAAATGGGGGCAAAATCTTGTAAGGCTCTA	873
121	Db	CGGATCCGGAGTGCACAGCACACCCTGGAGAAATGGGGGCAAAATCTTGTAAGGCTCTA	180
874	Qy	AGCCAGGAATCTGAATACTGCACAGATGGTCTTTGCATCTTAGATATAAAAAACCTCTTCAT	933
181	Db	AGCCAGGAATCTGAATACTGCACAGATGGTCTTTGCATCTTAG-----	223
934	Qy	GAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTCGTTTGTACTCGGGCTTGGGT	993
224	Db	-----GCATTGAGAATGCCAGCGACATTCGTTTGTACTCGGGCTTGGGT	267
994	Qy	GCTGCCGTCTGGCCGTGTGAGTCTCTGGTCAATTGGTGTACCCCTTTACACAGCGAGCCAG	1053
268	Db	GCTGCCGTCTGGCCGTGTGAGTCTCTGGTCAATTGGTGTACCCCTTTACACAGCGAGCCAG	327
1054	Qy	AGTGACTATGGCTGGAGCGTCAATTGACTCTTCTGCAATTGACAGGTGGCTTCCAGACCTTC	1113
328	Db	AGTGACTATGGCTGGAGCGTCAATTGACTCTTCTGCAATTGACAGGTGGCTTCCAGACCTTC	387
1114	Qy	AACTTCAAAACAGFCGCTCAAGCCAAAGATATCATGGAACTAATGATACAGAAATAATCC	1173
388	Db	AACTTCAAAACAGTCGCTCAAGCCAAAGATATCATGGAACTAATGATACAGAAATAATCC	447
1174	Qy	TTTTGTAATCCCTGCTCCCTGAATTCGCCATGCAGCCAGATCTGACAGTGAAGCCGGACA	1233
448	Db	TTTTGTAATCCCTGCTCCCTGAATTCGCCATGCAGCCAGATCTGACAGTGAAGCCGGACA	507
1234	Qy	TACAGCGGACCCATCTGCTGCGAGGACCTCTCGGACAAAGAGCTCATGACAGAGTCCCTCA	1293
508	Db	TACAGCGGACCCATCTGCTGCGAGGACCTCTCGGACAAAGAGCTCATGACAGAGTCCCTCA	567
1294	Qy	CTCTTTAAACCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTTCATGTTTCCCTG	1353
568	Db	CTCTTTAAACCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTTCATGTTTCCCTG	627
1354	Qy	GGAGTGTCTGAGAGAGCTGAGTAGCACGGCAAGAAATCAITCCAGGACTTTTCCCATGGA	1413
628	Db	GGAGTGTCTGAGAGAGCTGAGTAGCACGGCAAGAAATCAITCCAGGACTTTTCCCATGGA	687
1414	Qy	AACAACACACGCTTTAGTACAAATGCATCCCAAGAAATAAAATGCCCTACATCCAAAATCTG	1473
688	Db	AACAACACACGCTTTAGTACAAATGCATCCCAAGAAATAAAATGCCCTACATCCAAAATCTG	747
1474	Qy	TCATCACTCCCAACAGACAGAACTGAGGCAAACTGGTGTCTTTGGCCATTAGGGGGG	1533
748	Db	TCATCACTCCCAACAGACAGAACTGAGGCAAACTGGTGTCTTTGGCCATTAGGGGGG	807
1534	Qy	CGCTTAGTAATGCCAAATACACAGGGGTGAGCTTACTCATACACACGGTGCCATCCACAG	1593
808	Db	CGCTTAGTAATGCCAAATACACAGGGGTGAGCTTACTCATACACACGGTGCCATCCACAG	867
1594	Qy	GAGAAATCTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG	1640
868	Db	GAGAAATCTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG	914

Result No.	Score	Query		ID	Description
		Match	Length		
1	2736	100.0	2736	18	US-10-798-721-9
2	2736	100.0	3411	18	US-10-798-721-33
3	2660	97.2	2703	18	US-10-798-721-11
4	2642	96.6	2694	18	US-10-798-721-13
5	2566	93.8	2861	18	US-10-798-721-15
6	2320.8	84.8	8899	18	US-10-793-860-7444
7	2287	83.6	2979	18	US-10-473-518-136
8	2284	83.5	2868	19	US-10-872-681-55
9	2260	82.6	2898	17	US-10-094-886-115
10	2220	81.1	2661	19	US-10-872-681-53
11	2043	74.7	2043	18	US-10-798-721-25
					Sequence 9, Appli
					Sequence 33, Appl
					Sequence 11, Appl
					Sequence 13, Appl
					Sequence 15, Appl
					Sequence 7444, Ap
					Sequence 136, App
					Sequence 55, App
					Sequence 115, App
					Sequence 53, Appl
					Sequence 25, Appl

121 GCCTTCCCGAATCCATCCCATCAGTCTCCCTGGGACACTGCTCTCAATTTATAGAGGAGCCA 180  
 121 GCCTTCCCGAATCCATCCCATCAGTCTCCCTGGGACACTGCTCTCAATTTATAGAGGAGCCA 180  
 181 GATGATGCTTATATATCAAGAGCAACCCCTATTGCACTCAGGTGCAAGGAGGAGGAGGAGG 240  
 181 GATGATGCTTATATATCAAGAGCAACCCCTATTGCACTCAGGTGCAAGGAGGAGGAGGAGG 240  
 241 ATCAGATATCTTCAATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 241 ATCAGATATCTTCAATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 301 GAGACTCTGGACGAGAGCTCAGGTGTTGAAAGTCCGGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
 301 GAGACTCTGGACGAGAGCTCAGGTGTTGAAAGTCCGGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
 361 CAACAGGTGAGAGCTTCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 361 CAACAGGTGAGAGCTTCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 421 CACCTGGTACCTCCAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 421 CACCTGGTACCTCCAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 481 TTTGAAACAGACCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
 481 TTTGAAACAGACCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
 541 CGGCCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 541 CGGCCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 601 GACTCTGAAACAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 601 GACTCTGAAACAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGATGCGAGGAGGAGGAGGAGGAGGAGGAGG 720  
 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGATGCGAGGAGGAGGAGGAGGAGGAGGAGG 720  
 721 AGAAGCTCTGCGGACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
 721 AGAAGCTCTGCGGACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
 781 TGGTCCGCTGCGAGTCCAGAGTGTGAACATTTGCGGAGTCCGAGGAGGAGGAGGAGGAGG 840  
 781 TGGTCCGCTGCGAGTCCAGAGTGTGAACATTTGCGGAGTCCGAGGAGGAGGAGGAGGAGG 840  
 841 CCGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAAATCTGAAACTGCAAGAT 900  
 841 CCGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAAATCTGAAACTGCAAGAT 900  
 901 GGTCTTGTGATCTAGTAAACCTCTTCAATGAAATAAACCCCAAGAGGAGGAGGAGGAGG 960  
 901 GGTCTTGTGATCTAGTAAACCTCTTCAATGAAATAAACCCCAAGAGGAGGAGGAGGAGG 960  
 961 GCCAGGAGATCTGTTGATCTGGGCTTGGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTG 1020  
 961 GCCAGGAGATCTGTTGATCTGGGCTTGGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTG 1020  
 1021 GTCAATGGTGTACCTTTACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080  
 1021 GTCAATGGTGTACCTTTACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080  
 1081 TCTTCTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140  
 1081 TCTTCTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140  
 1141 AATATCATGAACTAATGATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200  
 1141 AATATCATGAACTAATGATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200

1201 GCCATGACCGCAGATCTGACAGTGGAGCCGAGCATACAGCGGAGCCCATCTGTCTGCGAGGAC 1260  
 1201 GCCATGACCGCAGATCTGACAGTGGAGCCGAGCATACAGCGGAGCCCATCTGTCTGCGAGGAC 1260  
 1261 CCTCTGGACAGGAGCTCATGACAGAGTCTCTACTCTTTTAAACCTTTTGGGAGCATCAAA 1320  
 1261 CCTCTGGACAGGAGCTCATGACAGAGTCTCTACTCTTTTAAACCTTTTGGGAGCATCAAA 1320  
 1321 GTGAAAGTCCAGAGCTCGTTTCTGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380  
 1321 GTGAAAGTCCAGAGCTCGTTTCTGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380  
 1381 GSCAAGATCAATCCAGGATTTTCCCATGGAACCAACACAGCTTTTATGATCAATGTCAT 1440  
 1381 GSCAAGATCAATCCAGGATTTTCCCATGGAACCAACACAGCTTTTATGATCAATGTCAT 1440  
 1441 CCCAGAAATAAATGCTTACATCCAAATCTGTCATCTCTCCCAAGAGGAGGAGGAGGAGG 1500  
 1441 CCCAGAAATAAATGCTTACATCCAAATCTGTCATCTCTCCCAAGAGGAGGAGGAGGAGG 1500  
 1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAAATGCAAAATACAGGGGTG 1560  
 1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAAATGCAAAATACAGGGGTG 1560  
 1561 AGCTTACTCATACACACAGCTGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620  
 1561 AGCTTACTCATACACACAGCTGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620  
 1621 ATCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680  
 1621 ATCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680  
 1681 GTCACTGTGGTCTCTCCAGACATGATCGTCAACCATCTTGGCATTGACCATCCCGGAC 1740  
 1681 GTCACTGTGGTCTCTCCAGACATGATCGTCAACCATCTTGGCATTGACCATCCCGGAC 1740  
 1741 TGTGAGATGTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800  
 1741 TGTGAGATGTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800  
 1801 AATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860  
 1801 AATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860  
 1861 CCTTTTGGTGTGATGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920  
 1861 CCTTTTGGTGTGATGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920  
 1921 ATCAGAGATGTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980  
 1921 ATCAGAGATGTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980  
 1981 TCCCTGGATTAACATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040  
 1981 TCCCTGGATTAACATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040  
 2041 GTGGTTTCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100  
 2041 GTGGTTTCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100  
 2101 TTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160  
 2101 TTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160  
 2161 AGAATTAACCACTTACTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220  
 2161 AGAATTAACCACTTACTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220  
 2221 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280  
 2221 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280  
 2281 TCTGCAAAATCTGATCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340

```
Db      2281  |||||TCTGCAAAATCTGCAATTCGGCAGCTCAAGGCCATGAAAGCCATGAAAGATCTTCCAAAGTGCAGACA 2340
Qy      2341  TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTTCTTCGCACAAAGAGGACAGCACTTTTC 2400
Db      2341  |||||TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTTCTTCGCACAAAGAGGACAGCACTTTTC 2400
Qy      2401  CCTGCACAGACTGGCCCCCAAGCCTTCAAAATTCCTTACTCCATCAGACAGCGGATTTGT 2460
Db      2401  CCTGCACAGACTGGCCCCCAAGCCTTCAAAATTCCTTACTCCATCAGACAGCGGATTTGT 2460
Qy      2461  GCTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
Db      2461  GCTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
Qy      2521  AGCATCAACAGGAATTTATCTTATTCGTGTACACAAAGTAGCCCATCTGCTGTCAATTTT 2580
Db      2521  AGCATCAACAGGAATTTATCTTATTCGTGTACACAAAGTAGCCCATCTGCTGTCAATTTT 2580
Qy      2581  AACTGTGGGAAGCTGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
Db      2581  AACTGTGGGAAGCTGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
Qy      2641  GAAGAGATTGGGAGGACACACAGAACTCTCAAACTTTAGAAATCCAGCTTTGATGAA 2700
Db      2641  GAAGAGATTGGGAGGACACACAGAACTCTCAAACTTTAGAAATCCAGCTTTGATGAA 2700
Qy      2701  GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
Db      2701  GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
```

## RESULT 2

```
US-10-798-721-33
; Sequence 33, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the Sa
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/10/798,721
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-721-33
```

```
Query Match 100.0%; Score 2736; DB 18; Length 3411;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGGAGAGCGCGCCACCGCAGGCGCGGCGGAGGCGCGCGCTCGCTCCCGTGG 60
Db      115  ATGGGAGAGCGCGCCACCGCAGGCGCGGCGGAGGCGCGCGCTCGCTCCCGTGG 174
Qy      61  CTGGGGCTGTGCTTCTGGGCGGAGGACCGCGCTCCCGAGGAACTGACAATGGCGAA 120
Db      175  CTGGGGCTGTGCTTCTGGGCGGAGGACCGCGCTCCCGAGGAACTGACAATGGCGAA 234
Qy      121  GCCCTTCCCGAATCCATCCATGCTCTCGGAGACATGCTCATTTTCATAGAGGCCA 180
Db      235  GCCCTTCCCGAATCCATCCATCAGCTCTCGGAGACATGCTCATTTTCATAGAGGCCA 294
Qy      181  GATGATGCTTATATTATCAAGACCAACCTATTGCACTCAGGTGCAAGCGAGCCAGCC 240
```

```
Db      295  GATGATGCTTATATTATCAAGACCAACCTATTGCACTCAGGTGCAAGCGAGCCAGCC 354
Qy      241  ATCCAGATATTTCTTCAAAATGCAACGCGAGTGGGTCCATCAGAACGAGACAGCTCTTGAA 300
Db      355  ATCCAGATATTTCTTCAAAATGCAACGCGAGTGGGTCCATCAGAACGAGACAGCTCTTGAA 414
Qy      301  GAGACTCTGACAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTTACTAGG 360
Db      415  GAGACTCTGACAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTTACTAGG 474
Qy      361  CAACAGGTGAGAGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCCGTGGAGC 420
Db      475  CAACAGGTGAGAGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCCGTGGAGC 534
Qy      421  CACTGCGGTACTCTCAAGAGCAGAAAGCCCTCTGTGCGCATAGCCTATTATCGGAAAAAC 480
Db      535  CACTGCGGTACTCTCAAGAGCAGAAAGCCCTCTGTGCGCATAGCCTATTATCGGAAAAAC 594
Qy      481  TTTTGAACAAGACCCACAAGGAAGGAGTTCCCATTTGAAGGCATGATTGTACTCAGTCGC 540
Db      595  TTTTGAACAAGACCCACAAGGAAGGAGTTCCCATTTGAAGGCATGATTGTACTCAGTCGC 654
Qy      541  CGCCCAACAGAGGAGTCCCTGCTGCGGAGTGGAAATGGCTGAAAAATGAAGAGCCCAT 600
Db      655  CGCCCAACAGAGGAGTCCCTGCTGCGGAGTGGAAATGGCTGAAAAATGAAGAGCCCAT 714
Qy      601  GACTCTGAACAAGACGAGAACATTTGACACAGAGGCTGACCATAACTTGATCATCAGGAG 660
Db      715  GACTCTGAACAAGACGAGAACATTTGACACAGAGGCTGACCATAACTTGATCATCAGGAG 774
Qy      661  GCACGGCTCTCGGACTCAGGAATTAACCTGTCATGCGAGCCACCATCGTGGCTTAAGAG 720
Db      775  GCACGGCTCTCGGACTCAGGAATTAACCTGTCATGCGAGCCACCATCGTGGCTTAAGAG 834
Qy      721  AGAAGCTCTGCGCCCACTGTTGTGGTCTACGTGGAGTGGAGTGGGAAGTGTGGAGCGAA 780
Db      835  AGAAGCTCTGCGCCCACTGTTGTGGTCTACGTGGAGTGGAGTGGGAAGTGTGGAGCGAA 894
Qy      781  TGTGCTGCTGTCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGACACACCC 840
Db      895  TGTGCTGCTGTCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGACACACCC 954
Qy      841  CCGAGAAATGGGGGCAAAATTTCTGGAAGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
Db      955  CCGAGAAATGGGGGCAAAATTTCTGGAAGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 1014
Qy      901  GGTCTTTGCACTCTAGATAAAAAACCTCTTATGAATAAAAAACCCCAAGCATTTGAGAAT 960
Db      1015  GGTCTTTGCACTCTAGATAAAAAACCTCTTATGAATAAAAAACCCCAAGCATTTGAGAT 1074
Qy      961  GCCAGGACATTTGCTTTGTAATCGGGCTTGGGTGCTGCGCTGCTGGCGCTTGCAGTCTG 1020
Db      1075  GCCAGGACATTTGCTTTGTAATCGGGCTTGGGTGCTGCGCTGCTGGCGCTTGCAGTCTG 1134
Qy      1021  GTCAATTTGGTGTCACTTTCACAGCGAGCCAGAGTGAATATGCGGTGGAGCTCATTTGAC 1080
Db      1135  GTCAATTTGGTGTCACTTTCACAGCGAGCCAGAGTGAATATGCGGTGGAGCTCATTTGAC 1194
Qy      1081  TCTTCTGCAATTTGACAGTGGCTTCCAGACCTTCAAACTTTCAAAAACAGTCCCGTCAAGCCAAG 1140
Db      1195  TCTTCTGCAATTTGACAGTGGCTTCCAGACCTTCAAACTTTCAAAAACAGTCCCGTCAAGCCAAG 1254
Qy      1141  AATATCATGAACTAATGATACAAAGAAAAATTCCTTTGGTGAATCTCCCTGCTCTGAAATCT 1200
Db      1255  AATATCATGAACTAATGATACAAAGAAAAATTCCTTTGGTGAATCTCCCTGCTCTGAAATCT 1314
Qy      1201  GCCATGCGAGCAGATCTGACAGTGGCGGACATACAGCGGACCCATCTCTCTCAGAGAC 1260
Db      1315  GCCATGCGAGCAGATCTGACAGTGGCGGACATACAGCGGACCCATCTCTCTCAGAGAC 1374
Qy      1261  CCTCTGAGCAAGGAGCTCATGACAGAGTCCCTCACTTTAAACCTTTGTCGAGCATCAAA 1320
Db      1375  CCTCTGAGCAAGGAGCTCATGACAGAGTCCCTCACTTTAAACCTTTGTCGAGCATCAAA 1434
```

QY 1321 GTGAAAGTCAGAGCTCGTTTCATGGTTTCCCTGGGAGTGTCTGAGAGCTGAGTACCAC 1380  
 Db 1435 GTGAAAGTCAGAGCTCGTTTCATGGTTTCCCTGGGAGTGTCTGAGAGCTGAGTACCAC 1494  
 QY 1381 GCGAAGATCATTTCCAGGACTTTTCCCATGGAAACACACAGCTTTTAGTACATGCAT 1440  
 Db 1495 GCGAGNATCATTTCCAGGACTTTTCCCATGGAAACACACAGCTTTTAGTACATGCAT 1554  
 QY 1441 CCAGAAATAAATGGCCCTACATCCAAATTCCTCATCTATCCCAAGAGCAGAACTG 1500  
 Db 1555 CCAGAAATAAATGGCCCTACATCCAAATTCCTCATCTATCCCAAGAGCAGAACTG 1614  
 QY 1501 AGACAACTGGTGTCTTTGGCAATTTAGGGGGGCTTAGTAAATGCAATACAGGGTG 1560  
 Db 1615 AGACAACTGGTGTCTTTGGCAATTTAGGGGGGCTTAGTAAATGCAATACAGGGTG 1674  
 QY 1561 AGCTTACTCATACACAGGTGCATCCACAGAGGAAATCTTGGGAGATTTATATGTCC 1620  
 Db 1675 AGCTTACTCATACACAGGTGCATCCACAGAGGAAATCTTGGGAGATTTATATGTCC 1734  
 QY 1621 ATCAACCAAGGTGAACCCAGCTCCAGTCCAGTCCAGTGTCTGAGTGTCTCTGAGTCTGAA 1680  
 Db 1735 ATCAACCAAGGTGAACCCAGCTCCAGTCCAGTCCAGTGTCTGAGTGTCTCTGAGTCTGAA 1794  
 QY 1681 GTCACTGTGTCTCCAGACATGATCGTCCACCACTCCCTTTTGCATTTGACATCCCGCAC 1740  
 Db 1795 GTCACTGTGTCTCCAGACATGATCGTCCACCACTCCCTTTTGCATTTGACATCCCGCAC 1854  
 QY 1741 TGTGCAGATGTCACTTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACAGCAGGGC 1800  
 Db 1855 TGTGCAGATGTCACTTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACAGCAGGGC 1914  
 QY 1801 AATGGAGAGAGTGTCTGAGTGAAGATGAATCTACATCTCTTACTGCTTTTGGAC 1860  
 Db 1915 AATGGAGAGAGTGTCTGAGTGAAGATGAATCTACATCTCTTACTGCTTTTGGAC 1974  
 QY 1861 CCCTTTCCGTGTCTATGCTCTGAGCAGCTTTGGGACCTATGCGCTCACTGAGAGGCCA 1920  
 Db 1975 CCCTTTCCGTGTCTATGCTCTGAGCAGCTTTGGGACCTATGCGCTCACTGAGAGGCCA 2034  
 QY 1921 ATCAACAGATGTGCGGTGAAGCAATCAAGTGGCGGTTTTTGGCTGCTATGCTGTAAAC 1980  
 Db 2035 ATCAACAGATGTGCGGTGAAGCAATCAAGTGGCGGTTTTTGGCTGCTATGCTGTAAAC 2094  
 QY 1981 TCCCTGTATTAACATTTGAGAGTTTACTGTGTGACATACCTCTGCTGATTTTCAGGAA 2040  
 Db 2095 TCCCTGTATTAACATTTGAGAGTTTACTGTGTGACATACCTCTGCTGATTTTCAGGAA 2154  
 QY 2041 GTGGTTTCAGATGAAGGCATCAAGTGGAGCAGCTCTGGAAGAACCAAAATTTGCTGCAT 2100  
 Db 2155 GTGGTTTCAGATGAAGGCATCAAGTGGAGCAGCTCTGGAAGAACCAAAATTTGCTGCAT 2214  
 QY 2101 TTCAAAGGGAATACCTTTAGTCTTTGAGATTTCTGCTTGAATATCCCTCCCATCTCTGTG 2160  
 Db 2215 TTCAAAGGGAATACCTTTAGTCTTTGAGATTTCTGCTTGAATATCCCTCCCATCTCTGTG 2274  
 QY 2161 AGAATTAACATTTCACTGCTGCTGAGAGTCCCGTTCTCCCGGTGTGTGAGTAAAC 2220  
 Db 2275 AGAATTAACATTTCACTGCTGCTGAGAGTCCCGTTCTCCCGGTGTGTGAGTAAAC 2334  
 QY 2221 CGGAGGCCCTTGCATGTGCTCTTCTCCCTGAGCGTTATAGCCCTCACTACCCAGCTG 2280  
 Db 2335 CGGAGGCCCTTGCATGTGCTCTTCTCCCTGAGCGTTATAGCCCTCACTACCCAGCTG 2394  
 QY 2281 TCCTGCAAAATCTGATTTGGCAGCTCAAGGCCATGAACAGATCTCTCAAGTGCAGACA 2340  
 Db 2395 TCCTGCAAAATCTGATTTGGCAGCTCAAGGCCATGAACAGATCTCTCAAGTGCAGACA 2454  
 QY 2341 TCAATCTTAGAGGTGAACGAGAAACCATCACTTTCTTCGACAAAGAGGACAGCACTTTC 2400  
 Db 2455 TCAATCTTAGAGGTGAACGAGAAACCATCACTTTCTTCGACAAAGAGGACAGCACTTTC 2514

QY 2401 CCTGCACAGACTGGCCCCCAAGCCCTTCAAAATTCCTACTCATCAGACAGCGGATTTGT 2460  
 Db 2515 CCTGCACAGACTGGCCCCCAAGCCCTTCAAAATTCCTACTCATCAGACAGCGGATTTGT 2574  
 QY 2461 GCTCATTTGATACCCCAATGCCAAAGGAGGAGTGGCAGATGTTAGCAGACAGAAAC 2520  
 Db 2575 GCTCATTTGATACCCCAATGCCAAAGGAGGAGTGGCAGATGTTAGCAGACAGAAAC 2634  
 QY 2521 AGCATCAACAGGAATTTATCTTATTTCTGCTACACAAAGTAGCCCATCTGCTGTCAATTTG 2580  
 Db 2635 AGCATCAACAGGAATTTATCTTATTTCTGCTACACAAAGTAGCCCATCTGCTGTCAATTTG 2694  
 QY 2581 AACCTGTGGAGCTGCTCATCAGCATGATGATGATCTGCTCCCTGGCTGTGCCCTT 2640  
 Db 2695 AACCTGTGGAGCTGCTCATCAGCATGATGATGATCTTGAATCCCTGGCTGTGCCCTT 2754  
 QY 2641 GAAGAGATTGGAGAGACACACAGCAAACTCTCAACATTTAGATCCAGCTTCATGAA 2700  
 Db 2755 GAAGAGATTGGAGAGACACACAGCAAACTCTCAACATTTAGATCCAGCTTCATGAA 2814  
 QY 2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736  
 Db 2815 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2850

RESULT 3

US-10-798-721-11  
 ; Sequence 11, Application US/10798721  
 ; Publication No. US20040248166A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the S  
 ; FILE REFERENCE: LEX-0244-USA  
 ; CURRENT APPLICATION NUMBER: US/10/798,721  
 ; CURRENT FILING DATE: 2004-03-11  
 ; PRIOR APPLICATION NUMBER: US/09/969,532  
 ; PRIOR FILING DATE: 2001-10-02  
 ; PRIOR APPLICATION NUMBER: US 60/237,280  
 ; PRIOR FILING DATE: 2000-10-02  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 11  
 ; LENGTH: 2703  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-10-798-721-11

Query Match 97.2%; Score 2660; DB 18; Length 2703;  
 Best Local Similarity 98.8%; Pred. No. 0;  
 Matches 2703; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 ATGGGGAGAGCGCGGCCACCGCAGCGCGCGGAGGGCGCGCGCTGGCTCCCGTGG 60  
 Db 1 ATGGGGAGAGCGCGGCCACCGCAGCGCGCGGAGGGCGCGCGCTGGCTCCCGTGG 60  
 QY 61 CTGGGGCTGTGCTTCTGGCGCGGAGGACCGCGGCTGCCCGAGGAATGCAATGCGCAA 120  
 Db 61 CTGGGGCTGTGCTTCTGGCGCGGAGGACCGCGGCTGCCCGAGGAATGCAATGCGCAA 120  
 QY 121 GCCCTTCCGATCCATCCATCAGCTCCTGGGACACTGCTCATTTTCATAGAGGAGCCA 180  
 Db 121 GCCCTTCCGGAATCCATCCATCAGCTCCTGGGACACTGCTCATTTTCATAGAGGAGCCA 180  
 QY 181 GATGATGCTTATATTAATCAAGAGCAACCTTATTTGCACTCAGGTGCAAAAGCGAGGCC 240  
 Db 181 GATGATGCTTATATTAATCAAGAGCAACCTTATTTGCACTCAGGTGCAAAAGCGAGGCC 240  
 QY 241 ATGCAGATATTTCTAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCAGCTCTCTGAA 300  
 Db 241 ATGCAGATATTTCTAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCAGCTCTCTGAA 300  
 QY 301 GAGACTCTGACGAGAGCTCAGGTTTGAAGTCCCGGAAGTGTTCATCAATGTTACTAGG 360



Db 301 |GAGCTCTGACGAGAGCTCAGGTTTGAGAGTCCGCGAGGTGTTTCATCAATGTTACTAGG 360  
Qy  
Db 361 |CAAAGGTGAGGACTTCCATGAGCCGAGGACTATTGGTCCAGTGTGTGGCGTGGAGC 420  
Db 361 |CAAAGGTGAGGACTTCCATGAGCCGAGGACTATTGGTCCAGTGTGTGGCGTGGAGC 420  
Qy 421 |CACCTGGGTACTCCRAAGACGAGAGGCTCTGTGTGGCATAGCCTATTATTACGGAANAAC 480  
Db 421 |CACCTGGGTACTCCRAAGACGAGAGGCTCTGTGTGGCATAGCCTATTATTACGGAANAAC 480  
Qy 481 |TTTGAACAAGACCCACAAGGAAGGAGTTCCCATTCGAAGGCATGATTGTACTGCACTGC 540  
Db 481 |TTTGAACAAGACCCACAAGGAAGGAGTTCCCATTCGAAGGCATGATTGTACTGCACTGC 540  
Qy 541 |CGCCACACAGAGGAGTCCCTGTCTGCGGAGGTGGAATGGCTGAAAAATGAAGAGCCCAT 600  
Db 541 |CGCCACACAGAGGAGTCCCTGTCTGCGGAGGTGGAATGGCTGAAAAATGAAGAGCCCAT 600  
Qy 601 |GACTCTGAAACAGACGAGAACATTGACACAGGAGTGAACCATTAACCTGATCATCAGGCAG 660  
Db 601 |GACTCTGAAACAGACGAGAACATTGACACAGGAGTGAACCATTAACCTGATCATCAGGCAG 660  
Qy 661 |GCACGGCTCTCGGACTCAGGAATTAACACCTGCATGCGAGCCACACATCGTGGCTAAGAGG 720  
Db 661 |GCACGGCTCTCGGACTCAGGAATTAACACCTGCATGCGAGCCACACATCGTGGCTAAGAGG 720  
Qy 721 |AGAAGCCTGTCCGCACTGTGTGTGCTCTACGTGAGTGGAGCTGGGAAGTGTGGAGCGAA 780  
Db 721 |AGAAGCCTGTCCGCACTGTGTGTGCTCTACGTGAGTGGAGCTGGGAAGTGTGGAGCGAA 780  
Qy 781 |TGGTCCGTCTGAGTCCAGAGTGAACATTGCGGATCCGGAAGTGAACAGACCAACCC 840  
Db 781 |TGGTCCGTCTGAGTCCAGAGTGAACATTGCGGATCCGGAAGTGAACAGACCAACCC 840  
Qy 841 |CCGAGAAATGGGGCAAAATCTGTGAAGTCTAAGCCAGGAATCTGAAACTGCACAGAT 900  
Db 841 |CCGAGAAATGGGGCAAAATCTGTGAAGTCTAAGCCAGGAATCTGAAACTGCACAGAT 900  
Qy 901 |GGTCTTTGCACTCTAGATAAAAAACCTCTTCATGAATAAAAAACCCAAAGCATTTGAGAAT 960  
Db 901 |GGTCTTTGCACTCTAG-----GCAATTGAGAAT 927  
Qy 961 |GCCAGCAATTTGTTGTTACTCGGGCTTGGGTGCTGCGCTCGTGGCGTTCGAGTCTTG 1020  
Db 928 |GCCAGCAATTTGTTGTTACTCGGGCTTGGGTGCTGCGCTCGTGGCGTTCGAGTCTTG 987  
Qy 1021 |GTCAATTGGTCTCACCTTTACAGAGGAGCCAGAGTCACTATGCGGTGGAGCTCATTTGAC 1080  
Db 988 |GTCAATTGGTCTCACCTTTACAGAGGAGCCAGAGTCACTATGCGGTGGAGCTCATTTGAC 1047  
Qy 1081 |TCTTCTGCATTGACAGTGGCTTCCAGACCTTCAACTTTCAAAAACAGTCCCGTCAAGCCAAAG 1140  
Db 1048 |TCTTCTGCATTGACAGTGGCTTCCAGACCTTCAACTTTCAAAAACAGTCCCGTCAAGCCAAAG 1107  
Qy 1141 |AATATCATGAACTAATGATACAGAAAAATTCCTTTGGTAACCTCCCTGCTCTCGAATTC 1200  
Db 1108 |AATATCATGAACTAATGATACAGAAAAATTCCTTTGGTAACCTCCCTGCTCTCGAATTC 1167  
Qy 1201 |GCCATGAGCCAGATCTGACAGTGGCCGACATACAGCGGACCCATCTGCTGCGAGGAC 1260  
Db 1168 |GCCATGAGCCAGATCTGACAGTGGCCGACATACAGCGGACCCATCTGCTGCGAGGAC 1227  
Qy 1261 |CCTCTGACAAAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTTGTGGACATCAAA 1320  
Db 1228 |CCTCTGACAAAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTTGTGGACATCAAA 1287  
Qy 1321 |GTGAAAGTCCAGAGCTCGTTCAAGTTTCCCTGGAGTGTCTGAGAGAGTGTGATACAC 1380  
Db 1288 |GTGAAAGTCCAGAGCTCGTTCAAGTTTCCCTGGAGTGTCTGAGAGAGTGTGATACAC 1347  
Qy 1381 |GGCAGAAATCATTTCCAGAGCTTTTCCCATGGAACCAACACAGCTTTTAGTCAATGCAT 1440

Db 1348 |GGCAAGAAATCATTTCCAGGACTTTTCCCATGGAACCAACACAGCTTTTAGTCAATGCAT 1407  
Qy 1441 |CCAGAAAAATAAATGOCCTACATCCAAAAATCTGTCACTCTCCCAACAAGACAGAACTG 1500  
Db 1408 |CCAGAAAAATAAATGOCCTACATCCAAAAATCTGTCACTCTCCCAACAAGACAGAACTG 1467  
Qy 1501 |AGGACAACTGGTCTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAATAACAGGGGTG 1560  
Db 1468 |AGGACAACTGGTCTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAATAACAGGGGTG 1527  
Qy 1561 |AGCTTACTCATACCAACACGGTGCATCCAGAGGAGAAATCTTTGGGAGATTTATATGTCC 1620  
Db 1528 |AGCTTACTCATACCAACACGGTGCATCCAGAGGAGAAATCTTTGGGAGATTTATATGTCC 1587  
Qy 1621 |ATCAACCAAGGTGAAACCCAGCTCCAGTCAATGGCTCTGAGGTCTCTGAGTCTCTGAA 1680  
Db 1588 |ATCAACCAAGGTGAAACCCAGCTCCAGTCAATGGCTCTGAGGTCTCTGAGTCTCTGAA 1647  
Qy 1681 |GTCACTGTGGTCTCCAGACATGATCGTCAACCTCCCTTTGCATTTGACATCCCGAC 1740  
Db 1648 |GTCACTGTGGTCTCCAGACATGATCGTCAACCTCCCTTTGCATTTGACATCCCGAC 1707  
Qy 1741 |TGTGCAGATGTCACTTCTGAGCAATGGAAATATCCATTTAAAGAAAGAGACACAGCAGGC 1800  
Db 1708 |TGTGCAGATGTCACTTCTGAGCAATGGAAATATCCATTTAAAGAAAGAGACACAGCAGGC 1767  
Qy 1801 |AAATGGAGAAATGATGTCACTGGAAGTGAATATCACTCTGTGTTACTGCTTTTGGAC 1860  
Db 1768 |AAATGGAGAAATGATGTCACTGGAAGTGAATATCACTCTGTGTTACTGCTTTTGGAC 1827  
Qy 1861 |CCCTTTGCGTGTCACTGCTCTGGACAGCTTTGGACCTATGCGCTCACTGGAGAGCCA 1920  
Db 1828 |CCCTTTGCGTGTCACTGCTCTGGACAGCTTTGGACCTATGCGCTCACTGGAGAGCCA 1887  
Qy 1921 |ATCACAGACTGTGCGGTGAAGCAACTGAAGTGGCGGTGTTTGGTGCATGTCTCTGAAC 1980  
Db 1888 |ATCACAGACTGTGCGGTGAAGCAACTGAAGTGGCGGTGTTTGGTGCATGTCTCTGAAC 1947  
Qy 1981 |TCCTGGATTAACAATTGAGAGTTACTGTGTGGACAATAACCTTTGTGATTTTCAGAA 2040  
Db 1948 |TCCTGGATTAACAATTGAGAGTTACTGTGTGGACAATAACCTTTGTGATTTTCAGAA 2007  
Qy 2041 |GTGTTTTCAGATGAAGGCAATCAAGTGGACAGCTCTGGAAGAACCAAAATTCCTGCAT 2100  
Db 2008 |GTGTTTTCAGATGAAGGCAATCAAGTGGACAGCTCTGGAAGAACCAAAATTCCTGCAT 2067  
Qy 2101 |TTCAAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCTCTGATATTCCTCCCATTCCTCTGG 2160  
Db 2068 |TTCAAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCTCTGATATTCCTCCCATTCCTCTGG 2127  
Qy 2161 |AGAATTAACCAATTCATCTGCTGCCAGGAAGTCCCGTTCTCCCGGTGTGGTGCAGTAAC 2220  
Db 2128 |AGAATTAACCAATTCATCTGCTGCCAGGAAGTCCCGTTCTCCCGGTGTGGTGCAGTAAC 2187  
Qy 2221 |CGGAGGCCCTGCATGTGCTCTCTCCCTGGAGGTTATAGCCCACTACCAACCCAGCTG 2280  
Db 2188 |CGGAGGCCCTGCATGTGCTCTCTCCCTGGAGGTTATAGCCCACTACCAACCCAGCTG 2247  
Qy 2281 |TCCTGCAAAATCTGCAATTCGGCAGCTCAAAAGGCAATGAACAGATCTCTCAAGTGCAGACA 2340  
Db 2248 |TCCTGCAAAATCTGCAATTCGGCAGCTCAAAAGGCAATGAACAGATCTCTCAAGTGCAGACA 2307  
Qy 2341 |TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTTCTTCGCAAGAGGACAGCACTTTC 2400  
Db 2308 |TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTTCTTCGCAAGAGGACAGCACTTTC 2367  
Qy 2401 |CCTGCAAGACTGGCCCAAGGCTTCAAAATTCCTTACTCTCATCAGACAGCGGATTTGT 2460  
Db 2368 |CCTGCAAGACTGGCCCAAGGCTTCAAAATTCCTTACTCTCATCAGACAGCGGATTTGT 2427  
Qy 2461 |GCTACATTTTCATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520  
Db 2428 |GCTACATTTTCATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2487

QY 2521 AGCATCAACAGGAATTTATCTTATTTCCGTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580  
 DB 2488 AGCATCAACAGGAATTTATCTTATTTCCGTACACAAAGTAGCCCATCTGCTGTCATTTTG 2547  
 QY 2581 AACCTGGGAAGCTCTCATACAGCATGATGTTGATCTTCACTCCCTGGCCTGTCGCCCTT 2640  
 DB 2548 AACCTGGGAAGCTCTCATACAGCATGATGTTGATCTTCACTCCCTGGCCTGTCGCCCTT 2607  
 QY 2641 GAAGAGATTGGGAGGACACACAGAACTCTCAACATTTTCAGAAATCCAGCTTGATGAA 2700  
 DB 2608 GAAGAGATTGGGAGGACACACAGAACTCTCAACATTTTCAGAAATCCAGCTTGATGAA 2667  
 QY 2701 GCGGACTTCAACTACAGCAGCGCAAAATGGACTCTAG 2736  
 DB 2668 GCGGACTTCAACTACAGCAGCGCAAAATGGACTCTAG 2703

RESULT 4  
 US-10-798-721-13  
 ; Sequence 13, Application US/10798721  
 ; Publication No. US20040248166A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the Sa  
 ; FILE REFERENCE: LEX-0244-USA  
 ; CURRENT APPLICATION NUMBER: US/10/798,721  
 ; CURRENT FILING DATE: 2004-03-11  
 ; PRIOR APPLICATION NUMBER: US/09/969,532  
 ; PRIOR FILING DATE: 2001-10-02  
 ; PRIOR APPLICATION NUMBER: US 60/237,280  
 ; PRIOR FILING DATE: 2000-10-02  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 2694  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-10-798-721-13

Query Match 96.6%; Score 2642; DB 18; Length 2694;  
 Best Local Similarity 98.5%; Pred. No. 0;  
 Matches 2694; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY 1 ATGGGAGAGCGCGGCCACCGCAGCGCGCGGAGGCGCGCGCTGCCGCTCCCGTGG 60  
 DB 1 ATGGGAGAGCGCGGCCACCGCAGCGCGCGGAGGCGCGCGCTGCCGCTCCCGTGG 60  
 QY 61 CTGGGGCTGTGCTTCTGGGCGGAGGACCGCGGCTGCCGCGGAACTGACAATGGCGAA 120  
 DB 61 CTGGGGCTGTGCTTCTGGGCGGAGGACCGCGGCTGCCGCGGAACTGACAATGGCGAA 120  
 QY 121 GCCCTTCCCGAATCCATCCATGCTCTGGGACACTGCTCATTTATAGAGAGGCCA 180  
 DB 121 GCCCTTCCCGAATCCATCCATGCTCTGGGACACTGCTCATTTATAGAGAGGCCA 180  
 QY 181 GATGATGCTTATATATCAAGAGCAACCTATTGCACTCAGGTGCAAGCGGCGCAGCC 240  
 DB 181 GATGATGCTTATATATCAAGAGCAACCTATTGCACTCAGGTGCAAGCGGCGCAGCC 240  
 QY 241 ATGCAGATATTTCTCAAAATCAACGGGAGTGGGTCCATCAGAACGAGCAGCTCTCTGAA 300  
 DB 241 ATGCAGATATTTCTCAAAATCAACGGGAGTGGGTCCATCAGAACGAGCAGCTCTCTGAA 300  
 QY 301 GAGACTCTGACAGAGCTCAGGTTTGAAGTCCGGAGTGTTCATCAATGTTACTAGG 360  
 DB 301 GAGACTCTGACAGAGCTCAGGTTTGAAGTCCGGAGTGTTCATCAATGTTACTAGG 360  
 QY 361 CAACAGGTGAGGACTTCCATGCGCGGAGGACTATTGGTCCAGTGTGGCGTGGAGC 420  
 DB 361 CAACAGGTGAGGACTTCCATGCGCGGAGGACTATTGGTCCAGTGTGGCGTGGAGC 420

QY 421 CACCTGGGTACCTCCCAAGAGCAGAAAGGCTCTGTGCGCATAGCCTATTATTACGAAAAAC 480  
 DB 421 CACCTGGGTACCTCCCAAGAGCAGAAAGGCTCTGTGCGCATAGCCTATTATTACGAAAAAC 480  
 QY 481 TTTGAAACAAGACCCACAAGGAAGGAAGTTCCCATTTGAAGGCATGATTTGCTACTGCTC 540  
 DB 481 TTTGAAACAAGACCCACAAGGAAGGAAGTTCCCATTTGAAGGCATGATTTGCTACTGCTC 540  
 QY 541 CGCCCAACAGAGGAGTCCCTGCTGCGGAGTGGAAATGGCTGAAATGAAGAGCCCATTT 600  
 DB 541 CGCCCAACAGAGGAGTCCCTGCTGCGGAGTGGAAATGGCTGAAATGAAGAGCCCATTT 600  
 QY 601 GACTCTGAAACAAGACCCACAAGGAAGGAAGTTCCCATTTGAAGGCATGATTTGCTACTG 660  
 DB 601 GACTCTGAAACAAGACCCACAAGGAAGGAAGTTCCCATTTGAAGGCATGATTTGCTACTG 660  
 QY 661 GACCGCTCTCGGACTCAGGAAATTAACAATGAGGAGCCAACTCGTGGCTAAGAGG 720  
 DB 661 GACCGCTCTCGGACTCAGGAAATTAACAATGAGGAGCCAACTCGTGGCTAAGAGG 720  
 QY 721 AGAAGCTCTGCGGCACTGTTGCTAGCTGAGTGGGAGCTGGGAAGTGTGGAGGAA 780  
 DB 721 AGAAGCTCTGCGGCACTGTTGCTAGCTGAGTGGGAGCTGGGAAGTGTGGAGGAA 780  
 QY 781 TGTCTCGTCTGCAAGTCCAGAGTGTGAACATTTTGGGATCCGGAGTGCAAGCACCACCC 840  
 DB 781 TGTCTCGTCTGCAAGTCCAGAGTGTGAACATTTTGGGATCCGGAGTGCAAGCACCACCC 840  
 QY 841 CCGAGAAATGGGGGCAAAATTTCTGTAAGGTCTAAGCCAGGAATCTGAAATCTGCACAGAT 900  
 DB 841 CCGAGAAATGGGGGCAAAATTTCTGTAAGGTCTAAGCCAGGAATCTGAAATCTGCACAGAT 900  
 QY 901 GGTCTTTGTCATCTAGATAAAACCTCTTCATGAATAAAACCCCAAGCAATTTGAGAAT 960  
 DB 901 GGTCTTTGTCATCTAGATAAAACCTCTTCATGAATAAAACCCCAAGCAATTTGAGAAT 960  
 QY 961 GCCAGCGACATTTGTTGATCTCGGCTTTGGGTGCTGCGGTGCTGGCGGTTGCGAGTCTG 1020  
 DB 961 GCCAGCGACATTTGTTGATCTCGGCTTTGGGTGCTGCGGTGCTGGCGGTTGCGAGTCTG 1020  
 QY 1021 GTCAATTTGGTGTACCCCTTTACAGACGGAGCAGAGTGAATGCGGTGGAGCTCATTTGAC 1080  
 DB 1021 GTCAATTTGGTGTACCCCTTTACAGACGGAGCAGAGTGAATGCGGTGGAGCTCATTTGAC 1080  
 QY 1081 TCTTCTGCAATTTGACAGTGGCTTCCAGACTTCAACTTCAAAACAGTCCGTCAAGCCAA 1140  
 DB 1081 TCTTCTGCAATTTGACAGTGGCTTCCAGACTTCAACTTCAAAACAGTCCGTCAAA----- 1134  
 QY 1141 AATATCATGGAACATAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAAATTT 1200  
 DB 1135 -----GGTAACTCCCTGCTCCTGAAATTTCT 1158  
 QY 1201 GCCATGCGGACATCTGACAGTGAAGCGGACATACAGCGGACCCATCTGTCTGCGAGGAC 1260  
 DB 1159 GCCATGCGGACATCTGACAGTGAAGCGGACATACAGCGGACCCATCTGTCTGCGAGGAC 1218  
 QY 1261 CCTCTGGAACAAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTGTGCGACATCAAA 1320  
 DB 1219 CCTCTGGAACAAGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTGTGCGACATCAAA 1278  
 QY 1321 GTGAAAGTCCAGAGCTCTGTTTCATGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380  
 DB 1279 GTGAAAGTCCAGAGCTCTGTTTCATGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1338  
 QY 1381 GGGCAAAATTCAGGAGCTTTTCCCATGGAAACAACACAGCTTTAGTACAATGTCAT 1440  
 DB 1339 GGGCAAAATTCAGGAGCTTTTCCCATGGAAACAACACAGCTTTAGTACAATGTCAT 1398  
 QY 1441 CCAGAGAAATAAATGCTTACATCCAAATCTGTCTCATCTCCCAAGAGCAGAACTG 1500  
 DB 1399 CCAGAGAAATAAATGCTTACATCCAAATCTGTCTCATCTCCCAAGAGCAGAACTG 1458  
 QY 1501 AGGACAACTGGTGTCTTTGGCCCAATTTAGGGGGGCGCTTAGTAAATGCAAAATACAGGGGTG 1560

Db	2539	AACTGTGGGAAGCTCGTCAATCAGCATGATGGTGATCTTGACTCCCTGGCGCTGTGCCCTT	2599
Qy	2641	GAAGAGATTGGGAGGACACACAGCAAACTCTCAAAACATTTTCAGAAATCCCAAGCTTGTATGAA	2700
Db	2599	GAAGAGATTGGGAGGACACACAGCAAACTCTCAAAACATTTTCAGAAATCCCAAGCTTGTATGAA	2658
Qy	2701	GCCGACTTCAACTACAGCAGCGCAAAATGGACTCTAG	2736
Db	2659	GCCGACTTCAACTACAGCAGCGCAAAATGGACTCTAG	2694

RESULT 5

US-10-798-721-15

Sequence 15, Application US/10798721

Publication No. US20040248166A1

GENERAL INFORMATION:

APPLICANT: Walke, D. Wade

APPLICANT: Scoville, John

TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoded

FILE REFERENCES: LEX-0244-USA

CURRENT APPLICATION NUMBER: US/10/798, 721

CURRENT FILING DATE: 2004-03-11

PRIOR APPLICATION NUMBER: US/09/969, 532

PRIOR FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: US 60/237, 280

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Fast-Seq for Windows Version 4.0

SEQ ID NO 15

LENGTH: 2661

TYPE: DNA

ORGANISM: homo sapiens

US-10-798-721-15

Query Match	93.8%	Score 2566;	DB 18;	Length 2661;
Best Local Similarity	97.3%	Pred. No. 0;		
Matches 2661;	Conservative	0;	Mismatches	0;
			Indels	75;
			Gaps	2;

Qy	1	ATGGGAGAGCGCGCGCCACCGCAGCGCGCGCGAGGGCGCGCGCTGGCTCCCGTGG	60
Db	1	ATGGGAGAGCGCGCGCCACCGCAGCGCGCGCGAGGGCGCGCGCTGGCTCCCGTGG	60
Qy	61	CTGGGCTGTGCTTCTGGGCGGAGGGAACCGCGCTGCCGAGAACTGACAAATGGCGAA	120
Db	61	CTGGGCTGTGCTTCTGGGCGGAGGACCGCGCTGCCGAGAACTGACAAATGGCGAA	120
Qy	121	GCCTTCCCAATCCATCCCATCAGCTCTCGGAGACATGCTCATTTTCATAGAGGAGCCA	180
Db	121	GCCTTCCCAATCCATCCCATCAGCTCTCGGAGACATGCTCATTTTCATAGAGGAGCCA	180
Qy	181	GATGATGCTTATATTAATCAAGAGCAACCTTATTTGCACTCAGGTTGCAAGCGAGGCCAGCC	240
Db	181	GATGATGCTTATATTAATCAAGAGCAACCTTATTTGCACTCAGGTTGCAAGCGAGGCCAGCC	240
Qy	241	ATGCAGATATTTTCAAAATCAACCGCGAGTGGGTCCATCAGAACGAGCAAGTCTCTGAA	300
Db	241	ATGCAGATATTTTCAAAATCAACCGCGAGTGGGTCCATCAGAACGAGCAAGTCTCTGAA	300
Qy	301	GAGACTTGACGAGAGCTCAGTTTGAAGGTCGCGAAGTGTTCATCAATGTTACTAGG	360
Db	301	GAGACTTGACGAGAGCTCAGTTTGAAGGTCGCGAAGTGTTCATCAATGTTACTAGG	360
Qy	361	CAACAGGTGAGGAGCTTCCATATGGCCCGAGGACTATTGGTGCACAGTGTGGCGTGGAGC	420
Db	361	CAACAGGTGAGGAGCTTCCATATGGCCCGAGGACTATTGGTGCACAGTGTGGCGTGGAGC	420
Qy	421	CACCTGGTACCTTCCAGAGCAGGAAGGCTCTGTGCGCATAGCCTATTACGGAATAAC	480
Db	421	CACCTGGTACCTTCCAGAGCAGGAAGGCTCTGTGCGCATAGCCTATTACGGAATAAC	480
Qy	481	TTTGAAACAAGACCCACAAGGAAGGAAGTTCCCATTTGAAGGCATGATGTGATCTGCACTGC	540
Db	481	TTTGAAACAAGACCCACAAGGAAGGAAGTTCCCATTTGAAGGCATGATGTGATCTGCACTGC	540

541 CGCCACCAAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCATT 600  
 Db |||||  
 541 CGCCACCAAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCATT 600  
 Qy |||||  
 601 GACTCTGAACAAGACAGAACTATGACACAGAGGCTGACCAATACCTGATCATCAGGCAG 660  
 Db |||||  
 601 GACTCTGAACAAGACAGAACTATGACACAGAGGCTGACCAATACCTGATCATCAGGCAG 660  
 Qy |||||  
 661 GCACGGCTCTCGGACTCAGGAATTAACCTGATCGCAGCCAACTCTGGCTAGAGG 720  
 Db |||||  
 661 GCACGGCTCTCGGACTCAGGAATTAACCTGATCGCAGCCAACTCTGGCTAGAGG 720  
 Qy |||||  
 721 AGAAGCTCTGCGCCACTGTTGTGGTCTAGCTGGAGTGGGAAGTGTGGAGCGAA 780  
 Db |||||  
 721 AGAAGCTCTGCGCCACTGTTGTGGTCTAGCTGGAGTGGGAAGTGTGGAGCGAA 780  
 Qy |||||  
 781 TGGTCCGTCTGAGTCCAGAGTGAACAATTTGCCGATCCGGAGTGCACAGCACCC 840  
 Db |||||  
 781 TGGTCCGTCTGAGTCCAGAGTGAACAATTTGCCGATCCGGAGTGCACAGCACCC 840  
 Qy |||||  
 841 CCAGAAATGGGGCAAAATCTGTGAAGTCTAAGCCAGGAATCTGAATCTGCACAGAT 900  
 Db |||||  
 841 CCAGAAATGGGGCAAAATCTGTGAAGTCTAAGCCAGGAATCTGAATCTGCACAGAT 900  
 Qy |||||  
 901 GGTCTTTGCAATCAAGTAAACCTCTTTCATGAATAAACCACCCCAAGCAATTTGAGAAT 960  
 Db |||||  
 901 GGTCTTTGCAATCAAGTAAACCTCTTTCATGAATAAACCACCCCAAGCAATTTGAGAAT 960  
 Qy |||||  
 961 GCACGAGCAATGCTTTGACTCGGGCTTGGGTGCTGCGGTGCTGGCGGTGCAATCTG 1020  
 Db |||||  
 961 GCACGAGCAATGCTTTGACTCGGGCTTGGGTGCTGCGGTGCTGGCGGTGCAATCTG 1020  
 Qy |||||  
 981 GTCAATGGTGTACCTTTACAGACGAGCCAGAGTACTATGGCGTGGACGCTCATTTGAC 1080  
 Db |||||  
 981 GTCAATGGTGTACCTTTACAGACGAGCCAGAGTACTATGGCGTGGACGCTCATTTGAC 1080  
 Qy |||||  
 1081 TCTTCTGCATTTGACAGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140  
 Db |||||  
 1081 TCTTCTGCATTTGACAGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140  
 Qy |||||  
 1141 AATATCATGAACTAATGATACAAGAAATCTTTGGTAACTCCCTGCTGCTGGAATTTCT 1200  
 Db |||||  
 1141 AATATCATGAACTAATGATACAAGAAATCTTTGGTAACTCCCTGCTGCTGGAATTTCT 1200  
 Qy |||||  
 1201 GCCATGAGCCAGATCTGACAGTGAGCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260  
 Db |||||  
 1201 GCCATGAGCCAGATCTGACAGTGAGCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260  
 Qy |||||  
 1261 CCTCTGGACAAGGAGTCTATGACAGAGTCTCTACTCTTTAAACCTTTTGGGACATCAAA 1320  
 Db |||||  
 1261 CCTCTGGACAAGGAGTCTATGACAGAGTCTCTACTCTTTAAACCTTTTGGGACATCAAA 1320  
 Qy |||||  
 1321 GTGAAAGTCCAGAGTCTGTTTCTGTTTCCCTGGAGTGTCTGAGAGCTGATGATACCAC 1380  
 Db |||||  
 1321 GTGAAAGTCCAGAGTCTGTTTCTGTTTCCCTGGAGTGTCTGAGAGCTGATGATACCAC 1380  
 Qy |||||  
 1381 GGCAGAACTCATTTCCAGGACTTTTCCCATGGAACCAACACAGCTTTTAGTACAATGCAT 1440  
 Db |||||  
 1381 GGCAGAACTCATTTCCAGGACTTTTCCCATGGAACCAACACAGCTTTTAGTACAATGCAT 1440  
 Qy |||||  
 1441 CCCAGAAATAAAATGCCCTACATCCAAATCTGTCTCATCTCCCTCCCAAGGACAGAACTG 1500  
 Db |||||  
 1441 CCCAGAAATAAAATGCCCTACATCCAAATCTGTCTCATCTCCCTCCCAAGGACAGAACTG 1500  
 Qy |||||  
 1501 AGGACAACTGCTGTTTGGCCATTTAGGGGGGCTGTAGTAATGCCAAATACAGGGGTG 1560  
 Db |||||  
 1501 AGGACAACTGCTGTTTGGCCATTTAGGGGGGCTGTAGTAATGCCAAATACAGGGGTG 1560  
 Qy |||||  
 1426 AGGACAACTGCTGTTTGGCCATTTAGGGGGGCTGTAGTAATGCCAAATACAGGGGTG 1485  
 Db |||||  
 1426 AGGACAACTGCTGTTTGGCCATTTAGGGGGGCTGTAGTAATGCCAAATACAGGGGTG 1485  
 Qy |||||  
 1561 AGCTTACTATACACAGTGCATCCAGAGGAGAAATTTCTTGGGAGATTTATATGTCC 1620  
 Db |||||  
 1561 AGCTTACTATACACAGTGCATCCAGAGGAGAAATTTCTTGGGAGATTTATATGTCC 1620  
 Qy |||||  
 1486 AGCTTACTATACACAGTGCATCCAGAGGAGAAATTTCTTGGGAGATTTATATGTCC 1545  
 Db |||||

1621 ATCAACCAAGGTGAACCCAGGCTCCAGTCAGATGGCTCTGAGGTGCTCTGAGTCTGAA 1680  
 Db |||||  
 1546 ATCAACCAAGGTGAACCCAGGCTCCAGTCAGATGGCTCTGAGGTGCTCTGAGTCTGAA 1605  
 Qy |||||  
 1681 GTCACTGTGGTCTCCAGACATGATCGTCAACCTCCCTTTGGATTGACCATCCGAC 1740  
 Db |||||  
 1606 GTCACTGTGGTCTCCAGACATGATCGTCAACCTCCCTTTGGATTGACCATCCGAC 1665  
 Qy |||||  
 1741 TGTGAGATGTCACTTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACAGCAGGCG 1800  
 Db |||||  
 1666 TGTGAGATGTCACTTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACAGCAGGCG 1725  
 Qy |||||  
 1801 AAATGGAGGAAGTGTGATGTCAGTGAAGATGAATCTAATCTCTGTTTGGCTTTGGAC 1860  
 Db |||||  
 1726 AAATGGAGGAAGTGTGATGTCAGTGAAGATGAATCTAATCTCTGTTTGGCTTTGGAC 1785  
 Qy |||||  
 1861 CCCTTTGGTGTGATGTCCTCTGACAGCTTTTGGGACCTATGCGCTCACTGGAGGCCA 1920  
 Db |||||  
 1786 CCCTTTGGTGTGATGTCCTCTGACAGCTTTTGGGACCTATGCGCTCACTGGAGGCCA 1845  
 Qy |||||  
 1921 ATCAAGACTGTGCGGTGAAGCAACTGAAGGTGGGGTGTGGCTGCTGATGCTCTGTAAC 1980  
 Db |||||  
 1846 ATCAAGACTGTGCGGTGAAGCAACTGAAGGTGGGGTGTGGCTGCTGATGCTCTGTAAC 1905  
 Qy |||||  
 1981 TCCCTGGATTAACAATTGAGATTTACTGTGTGGACAATACCCCTTGTGCTTTGAGAA 2040  
 Db |||||  
 1906 TCCCTGGATTAACAATTGAGATTTACTGTGTGGACAATACCCCTTGTGCTTTGAGAA 1965  
 Qy |||||  
 2041 GTGGTTTCAGATGAAGGCACTCAAGTGGACAGCTCTGGGAAGAACCAAAATTTGCTGAT 2100  
 Db |||||  
 1966 GTGGTTTCAGATGAAGGCACTCAAGTGGACAGCTCTGGGAAGAACCAAAATTTGCTGAT 2025  
 Qy |||||  
 2101 TTCAAGGGAATACCTTTAGTCTTTCAGATTTCTGTCTTGTGATTTCCCTTCTCTGG 2160  
 Db |||||  
 2026 TTCAAGGGAATACCTTTAGTCTTTCAGATTTCTGTCTTGTGATTTCCCTTCTCTGG 2085  
 Qy |||||  
 2161 AGAATTAACCAATTCATGCTGCGTGGCAAGTCCCGTCTCCCGGTGTGGTGCAGTAAC 2220  
 Db |||||  
 2086 AGAATTAACCAATTCATGCTGCGTGGCAAGTCCCGTCTCCCGGTGTGGTGCAGTAAC 2145  
 Qy |||||  
 2221 CGGAGCCCTGCTGCTGCTGCTTCCCTGGAGGCTTATACGCCCACTACCAACCCAGCTG 2280  
 Db |||||  
 2146 CGGAGCCCTGCTGCTGCTGCTTCCCTGGAGGCTTATACGCCCACTACCAACCCAGCTG 2205  
 Qy |||||  
 2281 TCTGCAAAATCTGATTCGGAGCTCAAGGCCATGAACAGATCCTTCAAGTGCAGACA 2340  
 Db |||||  
 2206 TCTGCAAAATCTGATTCGGAGCTCAAGGCCATGAACAGATCCTTCAAGTGCAGACA 2265  
 Qy |||||  
 2341 TCAATCTTAGAGTGAAGGAGAACCATCTTTCTTCCGACAGAGGACAGCACTTTC 2400  
 Db |||||  
 2266 TCAATCTTAGAGTGAAGGAGAACCATCTTTCTTCCGACAGAGGACAGCACTTTC 2325  
 Qy |||||  
 2401 CTGTCAGAGCTGGCCCAAGGCTTCAAAATTTCCCTACTCCATCAGAGAGGATTTGT 2460  
 Db |||||  
 2326 CTGTCAGAGCTGGCCCAAGGCTTCAAAATTTCCCTACTCCATCAGAGAGGATTTGT 2385  
 Qy |||||  
 2461 GCTACATTTGATACCCCAATTCGCAAGGCAAGGCTGGCAGATGTTAGCACAGAAAAAC 2520  
 Db |||||  
 2386 GCTACATTTGATACCCCAATTCGCAAGGCAAGGCTGGCAGATGTTAGCACAGAAAAAC 2445  
 Qy |||||  
 2521 AGCATCAACAGGAATTTATCTTTTTCGCTACAAGTAGGCCATCTGCTGATTTTG 2580  
 Db |||||  
 2446 AGCATCAACAGGAATTTATCTTTTTCGCTACAAGTAGGCCATCTGCTGATTTTG 2505  
 Qy |||||  
 2581 AACCTGTGGAGAGCTGCTCATCAGATGATGTTGATCTTTGACTCCCTGCGCTGTGCCCTT 2640  
 Db |||||  
 2506 AACCTGTGGAGAGCTGCTCATCAGATGATGTTGATCTTTGACTCCCTGCGCTGTGCCCTT 2565  
 Qy |||||  
 2641 GAAGAGATTTGGGAGGACACACAGCAAACTCTCAAACTTTGAGAAATTTCCAGCTTTGATGA 2700  
 Db |||||  
 2566 GAAGAGATTTGGGAGGACACACAGCAAACTCTCAAACTTTGAGAAATTTCCAGCTTTGATGA 2625  
 Qy |||||  
 2701 GCGGACTTCACTACAGGAGGCAAAATGGAATCTCTAG 2736

Db 2626 GCCGACTTCACTACAGCAGGCAAAATGGACTCTAG 2661  
|||||

## RESULT 6

US-10-723-860-7444  
; Sequence 7444, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7444  
; LENGTH: 8899  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (133)..(167)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2173)..(2189)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2947)..(2972)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (5055)..(5069)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (7333)..(7350)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-723-860-7444

Query Match 84.8%; Score 2320.8; DB 18; Length 8899;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 2552; Conservative 0; Mismatches 54; Indels 210; Gaps 2;  
QY 89 CCGCGGCTGCCGAGGAACTGACAAATGGCGAAGCCCTTCCGGAATCCATCCCATCAGCTC 148  
Db 129 CCANNN 188  
QY 149 CTGGGACATGCTCTATTCATGAGAGCCAGATGCTTATATCAAGAGCAACC 208  
Db 189 CTGGGACATGCTCTATTCATGAGAGCCAGATGCTTATATCAAGAGCAACC 248  
QY 209 CTATTCACATCAGGTGCAAGAGGAGCCAGCCATGAGATATCTTCAATGCAACGGCG 268  
Db 249 CTATTCACATCAGGTGCAAGAGGAGCCAGCCATGAGATATCTTCAATGCAACGGCG 308  
QY 269 AGTGGGTCCATCAGAACGACAGCTCTCTGAAGAGCTCTGGACGAGAGCTCAGGTTGA 328  
Db 309 AGTGGGTCCATCAGAACGACAGCTCTCTGAAGAGCTCTGGACGAGAGCTCAGGTTGA 368  
QY 329 AGTTCGGCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCG 388  
Db 369 AGTTCGGCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCG 428  
QY 389 AGGACTATTGGTCCAGTGTGGCGTGGAGCCACTGGGTACTCTCCAGAGCAGGAGG 448  
|||||

Db 429 AGGACTATTGGTCCAGTGTGGCGTGGAGCCACCTGGGTACTCTCAAGAGCAGGAAG 488  
QY 449 CCTCTGTGGCATAGCCTATTTTACGGAATAAATTTTGAACAAGACCCCAAGGAAGGAAG 508  
Db 489 CCTCTGTGGCATAGCCTATTTTACGGAATAAATTTTGAACAAGACCCCAAGGAAGGAAG 548  
QY 509 TTCCCATTTGAGGCATGATTGTACTGCACTGCGGCCACCAGAGGGAGTCCCTGCTCCG 568  
Db 549 TTCCCATTTGAGGCATGATTGTACTGCACTGCGGCCACCAGAGGGAGTCCCTGCTCCG 608  
QY 569 AGGTGAATGGCTGAAATAATGAAGAGCCATTGACTCTGAAACAAGACGAGAAATTTGACA 628  
Db 609 AGGTGAATGGCTGAAATAATGAAGAGCCATTGACTCTGAAACAAGACGAGAAATTTGACA 668  
QY 629 CAGGGCTGACCAATAACCTGATCATCAGGAGCAAGGCTCTCGGACTCAGGAAATTTACA 688  
Db 669 CAGGGCTGACCAATAACCTGATCATCAGGAGCAAGGCTCTCGGACTCAGGAAATTTACA 728  
QY 689 CTTGATGGGAGCAACATGCTGCTTAAGAGGAGAGCCCTGTCGGCCACTGTTGTGCTCT 748  
Db 729 CTTGATGGGAGCAACATGCTGCTTAAGAGGAGAGCCCTGTCGGCCACTGTTGTGCTCT 788  
QY 749 AC----- 750  
Db 789 ACGTGAATGGAGGCTGGTCTTCTCGACAGAGTGGTCAGCCTGCAATGTTGCTGTGTA 848  
QY 751 ----- 750  
Db 849 GAGGATGGCAGAAACGTTCCCGGACCTGACCAACCCAGCTCTCTCAATGTTGGGCGCT 908  
QY 751 -----GTGGATGGGA 760  
Db 909 TTTGTGAGGGAATGTCAGTGCAGAAATAACCTGCACCTTCTCTTTGTCTGTGGATGGGA 968  
QY 761 GCTGGGAAGTGTGGAGCAATGCTGCTGCAAGTCCAGAGTCCAGAACTTTTGGGATCC 820  
Db 969 GCTGGGAAGTGTGGAGCAATGCTGCTGCAAGTCCAGAGTCCAGAACTTTTGGGATCC 1028  
QY 821 GGGAGTGCACAGCACCAACCCCGAGAAATGGGGCAAAATTTCTGTGAAGTCTTAAGCCAGG 880  
Db 1029 GGGAGTGCACAGCACCAACCCCGAGAAATGGGGCAAAATTTCTGTGAAGTCTTAAGCCAGG 1088  
QY 881 AATCTGAAAACTGCACAGATGCTTTTGCATCTCTAGATAAAAAACCTCTTCTATGAATAA 940  
Db 1089 AATCTGAAAACTGCACAGATGCTTTTGCATCTCTAGATAAAAAACCTCTTCTATGAATAA 1148  
QY 941 AACCCCAAGAGCTTGAGAAATGCCAGAGCAATTCCTTTGTACTCGGGCTTGGGTGCTCCG 1000  
Db 1149 AACCCCAAGAGCTTGAGAAATGCCAGAGCAATTCCTTTGTACTCGGGCTTGGGTGCTCCG 1208  
QY 1001 TCGTGGCCGTTGCACTCTGCTGCTCAATTTGGTGTCAACCTTTTACAGCGAGCCAGAGTGA 1060  
Db 1209 TCGTGGCCGTTGCACTCTGCTGCTCAATTTGGTGTCAACCTTTTACAGCGAGCCAGAGTGA 1268  
QY 1061 ATGGCGTGGACGTCATTGACTCTTTGCAATTGACAGTGGCTTCCAGACCTTCAACTTCA 1120  
Db 1269 ATGGCGTGGACGTCATTGACTCTTTGCAATTGACAGTGGCTTCCAGACCTTCAACTTCA 1328  
QY 1121 AAACAGTCCGTCAAGCCAAAGAAATATCATGAACTAATGATACAAAGAAATCCTTTGCTGA 1180  
Db 1329 AAACAGTCCGTCAA-----GGTA 1346  
QY 1181 ACTCCCTGCTCTTGAATTTCTGCCATGCAGCCAGATCTGACAGTGGCGGACATACAGCG 1240  
Db 1347 ACTCCCTGCTCTTGAATTTCTGCCATGCAGCCAGATCTGACAGTGGCGGACATACAGCG 1406  
QY 1241 GACCCATCTGTCTGAGGACCTCTGGAAGAAGAGCTCATGACAGAGTCTCTACTCTTTA 1300  
Db 1407 GACCCATCTGTCTGAGGACCTCTGGAAGAAGAGCTCATGACAGAGTCTCTACTCTTTA 1466  
QY 1301 ACCCTTTTGTGGACATCAAGTGAAGTCCAGAGCTGCTTTCATGTTTCCCTGGGAGTGT 1360  
Db 1467 ACCCTTTTGTGGACATCAAGTGAAGTCCAGAGCTGCTTTCATGTTTCCCTGGGAGTGT 1526



1361 QY CTGAGAGAGCTGAGTACCAAGGCAAGAAATCATTCAGGACTTTTCCCATCGAACAACC 1420  
1527 Db CTGAGAGAGCTGAGTACCAAGGCAAGAAATCATTCAGGACTTTTCCCATCGAACAACC 1586  
1421 QY ACAGCTTTAGTCAATATGCAATCCAGAAATATAATGCCCTACATCAAAATCTGTATCAC 1480  
1587 Db ACAGCTTTAGTCAATATGCAATCCAGAAATATAATGCCCTACATCAAAATCTGTATCAC 1646  
1481 QY TCCCAACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAG 1540  
1647 Db TCCCAACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAG 1706  
1541 QY TAATGCCAATACAGGGGTGAGCTTACTCATACCAACCGTGCCATCCAGAGGAGAAAT 1600  
1707 Db TAATGCCAATACAGGGGTGAGCTTACTCATACCAACCGTGCCATCCAGAGGAGAAAT 1766  
1601 QY CTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCCTCCAGTCAGATGGCTCTG 1660  
1767 Db CTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCCTCCAGTCAGATGGCTCTG 1826  
1661 QY AGTGTCTCTGAGTCTGAGTCACTGTGTGCTCTCCAGACATGATCGTCAACACTCCCT 1720  
1827 Db AGTGTCTCTGAGTCTGAGTCACTGTGTGCTCTCCAGACATGATCGTCAACACTCCCT 1886  
1721 QY TTGCATTTGACATCCCGCACTGTCAGATGTCTAGTTCTGAGCAATTCGAATATCCATTTAA 1780  
1887 Db TTGCATTTGACATCCCGCACTGTCAGATGTCTAGTTCTGAGCAATTCGAATATCCATTTAA 1946  
1781 QY AGAAGAGGACACAGCAGGCAATGGAGGAAGTGTAGTCAAGTGAAGATGAATCTACAT 1840  
1947 Db AGAAGAGGACACAGCAGGCAATGGAGGAAGTGTAGTCAAGTGAAGATGAATCTACAT 2006  
1841 QY CTGTGTTACTGCTTTGGACCCCTTTGCGTGTCTATGCTCTGAGCACTTTGGGACCT 1900  
2007 Db CTGTGTTACTGCTTTGGACCCCTTTGCGTGTCTATGCTCTGAGCACTTTGGGACCT 2066  
1901 QY ATGGCTCTACTGGAGAGCAATCACAGCTGTGCGTGTCTATGCTCTGAGCACTTTGGGACCT 1960  
2067 Db ATGGCTCTACTGGAGAGCAATCACAGCTGTGCGTGTCTATGCTCTGAGCACTTTGGGACCT 2126  
1961 QY TTGCTGCTGCTCTGTAATCTCTGTAATCTCTGTAATCTCTGTAATCTCTGTAATCTCTG 2020  
2127 Db TTGCTGCTGCTCTGTAATCTCTGTAATCTCTGTAATCTCTGTAATCTCTGTAATCTCTG 2186  
2021 QY CCCCTTCTGCAATTCAGAGAGTGTCTTCCAGTGAAGGCAATCAAGTGGAGCTCTCTGG 2080  
2187 Db CCCCTTCTGCAATTCAGAGAGTGTCTTCCAGTGAAGGCAATCAAGTGGAGCTCTCTGG 2246  
2081 QY AAGAACCAAAATTCGTCATTTCAAGGGGAATACCTTTAGTCTTTTCAAGTCTTCTGCTCTG 2140  
2247 Db AAGAACCAAAATTCGTCATTTCAAGGGGAATACCTTTAGTCTTTTCAAGTCTTCTGCTCTG 2306  
2141 QY ATATTCGCCCATTCCTCTGAGAAATTAACCAATTCACCTGCTGCGAGAGTCCCGTTCT 2200  
2307 Db ATATTCGCCCATTCCTCTGAGAAATTAACCAATTCACCTGCTGCGAGAGTCCCGTTCT 2366  
2201 QY CCCCGTGTGTGAGTAACCGGAGCCCTGCACTGTGCTCTCTCTGAGAGTGTATATA 2260  
2367 Db CCCCGTGTGTGAGTAACCGGAGCCCTGCACTGTGCTCTCTCTGAGAGTGTATATA 2426  
2261 QY CGCCCACTACCAACCGAGCTGTCTGCAAAATCTGCAATTCGCGAGCTCAAGGCCATGAAC 2320  
2427 Db CGCCCACTACCAACCGAGCTGTCTGCAAAATCTGCAATTCGCGAGCTCAAGGCCATGAAC 2486  
2321 QY AGATCTTCAAGTGCAGACATCAATCTTAGAGAGTGAACGAGAAACCATCTCTTCTTCG 2380  
2487 Db AGATCTTCAAGTGCAGACATCAATCTTAGAGAGTGAACGAGAAACCATCTCTTCTTCG 2546  
2381 QY CACAAGAGGACAGCACTTTCCCTGCAAGAGCTGGCCCCCAAGCCCTTCAAAATCCCTACT 2440  
2547 Db CACAAGAGGACAGCACTTTCCCTGCAAGAGCTGGCCCCCAAGCCCTTCAAAATCCCTACT 2606

RESULT 7

US-10-473-518-136  
; Sequence 136, Application US/10473518  
; Publication No. US20040138416A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE CORPORATION  
; APPLICANT: THORNTON, Michael B.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: RICHARDSON, Thomas W.  
; APPLICANT: SWARNAKAR, Anita  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: ISON, Craig H.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: HAFALIA, April J.A.  
; APPLICANT: AU-YOUNG, Janice K.  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: KHAN, Farrah A.  
; APPLICANT: BECHA, Shanya D.  
; APPLICANT: LU, Yan  
; APPLICANT: ARVIZU, Chandra S.  
; APPLICANT: BOROWSKY, Mark L.  
; APPLICANT: LAL, Preeti G.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: EMERLING, Brooke M.  
; APPLICANT: WALSH, Roderick T.  
; APPLICANT: YUE, Henry  
; APPLICANT: BURFORD, Neil  
; APPLICANT: GRAUL, Richard C.  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: PF-0933 USN  
; CURRENT APPLICATION NUMBER: US/10/473,518  
; CURRENT FILING DATE: 2003-09-30  
; PRIOR APPLICATION NUMBER: PCT/US02/09923  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/287,266  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/285,336  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: US 60/283,714  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/280,683  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 146  
; SOFTWARE: PERL Program  
; SEQ ID NO 136  
; LENGTH: 2979  
; TYPE: DNA  
; ORGANISM: Homo sapiens

2441 QY CCATCAGACAGCGGATTTGTGTACATTTGATACCCCAATGCCAAAGGCAAGACTGGC 2500  
2607 Db CCATCAGACAGCGGATTTGTGTACATTTGATACCCCAATGCCAAAGGCAAGACTGGC 2666  
2501 QY AGATGTTAGCACAGAAAACAGCATCAACAGGAATTTATCTTATTTCTGCTACACAAAGTA 2560  
2667 Db AGATGTTAGCACAGAAAACAGCATCAACAGGAATTTATCTTATTTGCTTACACAAAGTA 2726  
2561 QY GCCCATCTGCTGTCTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGTCTTG 2620  
2727 Db GCCCATCTGCTGTCTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGTCTTG 2786  
2621 QY ACTCCCTGGCCTGTGCTTGAAGAGATTGGAGGACACACACGAAACTCTCAAAACATTT 2680  
2787 Db ACTCCCTGGCCTGTGCTTGAAGAGATTGGAGGACACACACGAAACTCTCAAAACATTT 2846  
2681 QY CAGATCCCACTGTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGAATCTCTAG 2736  
2847 Db CAGATCCCACTGTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGAATCTCTAG 2902





```

Db 2178 CTGTAACCTCCGATGATCAACTTGGAGTTTACTGTGGCAATACCCCTTGTGCATT 2237
QY 2034 TCAGGAAGTGGTTTCAGATGAAGGATCAAGGTGGAGAGCTCCCTGGGAAGAACCAAAATT 2093
Db 2238 TCAGGAAGTGGTTTCAGATGAAGGATCAAGGTGGAGAGCTCCCTGGGAAGAACCAAAATT 2297
QY 2094 GCTGCAATTTCAAGGAATACCTTTAGTCTTTCAGATTTCTGATTTCTGATTTCCCCCAATT 2153
Db 2298 GCTGCAATTTCAAGGAATACCTTTAGTCTTTCAGATTTCTGATTTCTGATTTCCCCCAATT 2357
QY 2154 CTTCTGGAGAAATTAACCAATTCATGCTCCCTGCGAGAAATCCCGTCTCTCCCGGTGGTG 2213
Db 2358 CTTCTGGAGAAATTAACCAATTCATGCTCCCTGCGAGAAATCCCGTCTCTCCCGGTGGTG 2417
QY 2214 CAGTAACCGGAGCCCTGCACTGTGCTTCTCCCTGGAGAGTTATACGCCCACTACAC 2273
Db 2418 CAGTAACCGGAGCCCTGCACTGTGCTTCTCCCTGGAGAGTTATACGCCCACTACAC 2477
QY 2274 CCAGCTGTCTCCCAATCTGATTCGGGAGCTCAAGGCCATGAACAGATCTTCAAGT 2333
Db 2478 CCAGCTGTCTCCCAATCTGATTCGGGAGCTCAAGGCCATGAACAGATCTTCAAGT 2537
QY 2334 GCAGACATCAATCTAGAGAGTGAACGAGAAACCAATCACTTTCTTCGCAACAGAGACAG 2393
Db 2538 GCAGACATCAATCTAGAGAGTGAACGAGAAACCAATCACTTTCTTCGCAACAGAGACAG 2597
QY 2394 CACTTTCCCTGCAAGCTGGGCCCAAGCTTCAAAATTCCTACTCCATCAGACAGCG 2453
Db 2598 CACTTTCCCTGCAAGCTGGGCCCAAGCTTCAAAATTCCTACTCCATCAGACAGCG 2657
QY 2454 GATTTGCTGTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCACA 2513
Db 2658 GATTTGCTGTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCACA 2717
QY 2514 GAAAAACAGCATCAACAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCTCTGCTGT 2573
Db 2718 GAAAAACAGCATCAACAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCTCTGCTGT 2777
QY 2574 CATTGTAACCTGTGGAGCTGTCATCAGCATGATGTTGATCTTGTGCTCCCTGGCCCTG 2633
Db 2778 CATTGTAACCTGTGGAGCTGTCATCAGCATGATGTTGATCTTGTGCTCCCTGGCCCTG 2837
QY 2634 TGCCCTTGAAGAGATTGGGAGGACACACAGAACTCTCAAAATTTCAAGATCCCAAGCT 2693
Db 2838 TGCCCTTGAAGAGATTGGGAGGACACACAGAACTCTCAAAATTTCAAGATCCCAAGCT 2897
QY 2694 TGATGAAGCCGACTTCAACTACAGCGGCAAAATGGACTCTAG 2736
Db 2898 TGATGAAGCCGACTTCAACTACAGCGGCAAAATGGACTCTAG 2940

```

RESULT 8

```

US-10-872-681-55
; Sequence 55, Application US/10872681
; Publication No. US20050026251A1
; GENERAL INFORMATION:
; APPLICANT: ARES TRADING LIMITED
; TITLE OF INVENTION: TRANSMEMBRANE PROTEIN
; FILE REFERENCE: P029209W0
; CURRENT APPLICATION NUMBER: US/10/872,681
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: GB0130721.4
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 55
; LENGTH: 2868
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SEQ ID NO:33
US-10-872-681-55

```

```

Query Match 83.5%; Score 2284; DB 19; Length 2868;
Best Local Similarity 91.3%; Pred. No. 0;
Matches 2557; Conservative 0; Mismatches 0; Indels 243; Gaps 3;

QY 102 AGGAACATGCAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCTCTGGGACACTGCC 161
Db 144 AGGAACATGCAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCTCTGGGACACTGCC 203
QY 162 TCATTTTATAGAGGAGCCAGATGATGCTTATATATATCAAGAGCAACCTTATTGCACTCAG 221
Db 204 TCATTTTATAGAGGAGCCAGATGATGCTTATATATATCAAGAGCAACCTTATTGCACTCAG 263
QY 222 GTGCAAAACGAGGCGCAGCATGTCATATTTCTTCAAAATGCAACGCGGAGTGGGTCCATCA 281
Db 264 GTGCAAAACGAGGCGCAGCATGTCATATTTCTTCAAAATGCAACGCGGAGTGGGTCCATCA 323
QY 282 GAAACGAGCACGCTCTCTGAAGAGACTCTGGAAGAGAGCTCAGTTTGAAGGTCGGGAAAGT 341
Db 324 GAAACGAGCACGCTCTCTGAAGAGACTCTGGAAGAGAGCTCAGTTTGAAGGTCGGGAAAGT 383
QY 342 GTTTCATCAATGTTACTTAGGCAACAGTGGAGACTTCCATGGGCCCGGAGGACTATTGGTG 401
Db 384 GTTTCATCAATGTTACTTAGGCAACAGTGGAGACTTCCATGGGCCCGGAGGACTATTGGTG 443
QY 402 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTTCAAGAGCAGGAAGGCTCTGTGCGCAT 461
Db 444 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTTCAAGAGCAGGAAGGCTCTGTGCGCAT 503
QY 462 AGCCTATTATTCGGAAGAACTTTGAAACAAGACCCACAGGAAGGGAAGTTCCTATTGAGG 521
Db 504 AGCCTATTATTCGGAAGAACTTTGAAACAAGACCCACAGGAAGGGAAGTTCCTATTGAGG 563
QY 522 CATGATTTGCTGCTGCTGCGCCACAGAGGAGTCCCTGCTGCGGAGTGGATGGCT 581
Db 564 CATGATTTGCTGCTGCTGCGCCACAGAGGAGTCCCTGCTGCGGAGTGGATGGCT 623
QY 582 GAAAAATGAAGAGCCCATTTGACTCTTGAACAAGACGAGAACATTTGACACAGGGCTGACCA 641
Db 624 GAAAAATGAAGAGCCCATTTGACTCTTGAACAAGACGAGAACATTTGACACAGGGCTGACCA 683
QY 642 TAACTGATCATCAGGAGGAGCCGCTCTCGAGCTCAGGAATTAACCTGATGATGCGAGC 701
Db 684 TAACTGATCATCAGGAGGAGCCGCTCTCGAGCTCAGGAATTAACCTGATGATGCGAGC 743
QY 702 CAACATCGTGGCTAAGAGAGGAGGAGCTCTGCGCCACTGTTGTGGTCTAC----- 750
Db 744 CAACATCGTGGCTAAGAGAGGAGGAGCTCTGCGCCACTGTTGTGGTCTACCGTGAATGGAGG 803
QY 751 ----- 750
Db 804 CTGGTCTTCTCGACAGAGTGGTGGTCAATGTTCTGCTGTGTAGAGGATGGCAGAA 863
QY 751 ----- 750
Db 864 ACGTTCCTCGGACCTGCAACCAACCCAGCTCTCTCAATGTGTGGGCCCTTTTGTGAGGGAAT 923
QY 751 -----GTGGATGGGAGCTGGGAAGTGTG 773
Db 924 GTCACTGTCAGAAAAATAACCTGCACCTTCTTTGCTCTGCTGGATGGGAGCTGGGAAGTGTG 983
QY 774 GAGCGAATGGTCTGCTGAGTCCAGAGTGAACATTTGCGGATCCGGAGTCCGGAGTGCACAGC 833
Db 984 GAGCGAATGGTCTGCTGAGTCCAGAGTGAACATTTGCGGATCCGGAGTCCGGAGTGCACAGC 1043
QY 834 ACCACCCCGAGAAATGGGGGCAAAATTTCTGTGAAGGTCTAAGCCAGGAATCTGAAACCTG 893
Db 1044 ACCACCCCGAGAAATGGGGGCAAAATTTCTGTGAAGGTCTAAGCCAGGAATCTGAAACCTG 1103
QY 894 CACAGATGGTCTTTGATCCTTAGATAAAAAAAGCTCTTTCATGAATAAAAAACCCCAAGCAT 953
Db 1104 CACAGATGGTCTTTGATCCTTAG-----GCAT 1130

```

QY 954 TGAGAAATGCCAGGACATTCCTTTGTAATCGGGCTTGGGTGCTGCCGTGCGCGTTC 1013  
DB 1131 TGAGAAATGCCAGGACATTCCTTTGTAATCGGGCTTGGGTGCTGCCGTGCGCGTTC 1190  
QY 1014 AGTCCCTGGTCAATGGTGTCAACCCCTTTACAGACGGAGCCAGAGTGACTATATGGCGTGGACGT 1073  
DB 1191 AGTCCCTGGTCAATGGTGTCAACCCCTTTACAGACGGAGCCAGAGTGACTATATGGCGTGGACGT 1250  
QY 1074 CATTTGACTCTTGTGATGTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCA 1133  
DB 1251 CATTTGACTCTTGTGATGTGACAGGTGGCTTCCAGACCTTCAAAACAGTCCGTCA 1310  
QY 1134 AGCAAGAAATATCATGGAATCAATGATACAGAAATATCTTTGGTAACTCCCTGCTCCT 1193  
DB 1311 A-----GGTAACTCCCTGCTCCT 1328  
QY 1194 GAATTTCTGCCATGCAGCAGATCTGACAGTGAGCCGACATACAGCGGACCCATCTGTCT 1253  
DB 1329 GAATTTCTGCCATGCAGCAGATCTGACAGTGAGCCGACATACAGCGGACCCATCTGTCT 1388  
QY 1254 GCAGGACCTCTGGACAAGAGCTCATGACAGAGTCTCTCACTCTTTAAACCCCTTTGCGGA 1313  
DB 1389 GCAGGACCTCTGGACAAGAGCTCATGACAGAGTCTCTCACTCTTTAAACCCCTTTGCGGA 1448  
QY 1314 CATCAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGAGTGTCTGAGAGCTGA 1373  
DB 1449 CATCAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGAGTGTCTGAGAGCTGA 1508  
QY 1374 GTACACCGGCAAGAAATCATTTCCAGGACTTTTCCCATGGAAACAAACACAGCTTTAGTAC 1433  
DB 1509 GTACACCGGCAAGAAATCATTTCCAGGACTTTTCCCATGGAAACAAACACAGCTTTAGTAC 1568  
QY 1434 AATGCAATCCAGAAATAAATGCGCTACATCCAAATCTGTCACTCCCAACAGGAC 1493  
DB 1569 AATGCAATCCAGAAATAAATGCGCTACATCCAAATCTGTCACTCCCAACAGGAC 1628  
QY 1494 AGAACTGAGCAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAATAC 1553  
DB 1629 AGAACTGAGCAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAATAC 1688  
QY 1554 AGGGGTGAGCTTACTCATACACACGGTGCCATCCAGAGAGAGAAATCTTTGGGAGATTGA 1613  
DB 1689 AGGGGTGAGCTTACTCATACACACGGTGCCATCCAGAGAGAGAAATCTTTGGGAGATTGA 1748  
QY 1614 TATGTCCATCAACCAAGGTGAACCCAGCTCCAGTCAAGTGGCTGTGAGGTGCTCCTGAG 1673  
DB 1749 TATGTCCATCAACCAAGGTGAACCCAGCTCCAGTCAAGTGGCTGTGAGGTGCTCCTGAG 1808  
QY 1674 TCTGAACTCACTGGTGTCTCCAGACATGATCGTCACCACTCCCTTTGCAATGACCAT 1733  
DB 1809 TCTGAACTCACTGGTGTCTCCAGACATGATCGTCACCACTCCCTTTGCAATGACCAT 1868  
QY 1734 CCGCACTGTGCAGATGTGAGTGTCTGAGCAATGGAATATCATTTAAAGAGAGGACACA 1793  
DB 1869 CCGCACTGTGCAGATGTGAGTGTCTGAGCAATGGAATATCATTTAAAGAGAGGACACA 1928  
QY 1794 GCAGGGCAATGGGAGGAAGTGTGATGAGTGGAGATGAATCTATCACTCTGTTACTGCTC 1853  
DB 1929 GCAGGGCAATGGGAGGAAGTGTGATGAGTGGAGATGAATCTATCACTCTGTTACTGCTC 1988  
QY 1854 TTTGGACCCCTTTGCGTGTATGTCTCCCTGGACAGCTTTGGGACCTATGCGCTCACTGG 1913  
DB 1989 TTTGGACCCCTTTGCGTGTATGTCTCCCTGGACAGCTTTGGGACCTATGCGCTCACTGG 2048  
QY 1914 AGAGCCAAATCAAGCTGCGGTGAAGCAACTGAAGTGGCGGTGCTGGCTGCAATGTC 1973  
DB 2049 AGAGCCAAATCAAGCTGCGGTGAAGCAACTGAAGTGGCGGTGCTGGCTGCAATGTC 2108  
QY 1974 CTGTAACTCCCTGGATTAACAATCTTGAGATTTTACTGTGTGGACAATAACCCCTTTGTGCATT 2033  
DB 2109 CTGTAACTCCCTGGATTAACAATCTTGAGATTTTACTGTGTGGACAATAACCCCTTTGTGCATT 2168  
QY 2034 TCAGGAAGTGGTTTCAGATGAAGGCAATCAAGGTGGACAGCTCTCTGGAAGAACCAAAAT 2093

DB 2169 TCAGGAAGTGGTTTCAGATGAAGGCAATCAAGGTGGACAGCTCTGGAAGAACCAAAAT 2228  
QY 2094 GCTGCATTTCAAAGGGAATACCTTTAGTCTTTCAGATTTCTGTCTTGTATTTCCCCCAATT 2153  
DB 2229 GCTGCATTTCAAAGGGAATACCTTTAGTCTTTCAGATTTCTGTCTTGTATTTCCCCCAATT 2288  
QY 2154 CCTCTGGAGAAATTAACCAATTCAGTCCCTGCCAGGAAGTCCCGTTCTCCCGCGTGGTG 2213  
DB 2289 CCTCTGGAGAAATTAACCAATTCAGTCCCTGCCAGGAAGTCCCGTTCTCCCGCGTGGTG 2348  
QY 2214 CAGTAACCGGACGCCCTGCACTGTCTTCTCCCTGGAGCGTTATACGCCCACTACAC 2273  
DB 2349 CAGTAACCGGACGCCCTGCACTGTCTTCTCCCTGGAGCGTTATACGCCCACTACAC 2408  
QY 2274 CCAAGTGTCTGCAAAATCTGCATTCGGCAGCTCAAGGGCCATGAACAGATCTCCCAAGT 2333  
DB 2409 CCAAGTGTCTGCAAAATCTGCATTCGGCAGCTCAAGGGCCATGAACAGATCTCCCAAGT 2468  
QY 2334 GCAGACATCAATCTTAGAGAGTGAACGAGAAACCATCATCTTTCTCCCAAGAGGACAG 2393  
DB 2469 GCAGACATCAATCTTAGAGAGTGAACGAGAAACCATCATCTTTCTCCCAAGAGGACAG 2528  
QY 2394 CACTTTCCCTGACAGACTGCGCCCAAGGCTTCAAAATTTCCCTACTCCATCAGACAGCG 2453  
DB 2529 CACTTTCCCTGACAGACTGCGCCCAAGGCTTCAAAATTTCCCTACTCCATCAGACAGCG 2588  
QY 2454 GATTTGTGTCTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCACA 2513  
DB 2589 GATTTGTGTCTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGTTAGCACA 2648  
QY 2514 GAAAAACAGATCAACAGGAAATTTATCTTATTTCCGCTACACAAAGTAGGCCATCTGCTGT 2573  
DB 2649 GAAAAACAGATCAACAGGAAATTTATCTTATTTCCGCTACACAAAGTAGGCCATCTGCTGT 2708  
QY 2574 CATTTTGAACCTGTGGAGCTCGTCAATCAGCATGATGATGATCTTCACTCCCTGGCGTG 2633  
DB 2709 CATTTTGAACCTGTGGAGCTCGTCAATCAGCATGATGATGATCTTCACTCCCTGGCGTG 2768  
QY 2634 TGCCCTTGAAGAGATGGGAGGACACACAGAAATCTCTCAAAATTTTCAAAATTTCCAGATCCCAAGT 2693  
DB 2769 TGCCCTTGAAGAGATGGGAGGACACACAGAAATCTCTCAAAATTTTCAAAATTTCCAGATCCCAAGT 2828  
QY 2694 TGATGAAGCCGACTTCAATCAGACGCGGCAAAATGACTC 2733  
DB 2829 TGATGAAGCCGACTTCAATCAGACGCGGCAAAATGACTC 2868

## RESULT 9

US-10-094-886-115  
; Sequence 115, Application US/10094886  
; Publication No. US20040002120A1  
; GENERAL INFORMATION:  
; APPLICANT: Kkuda, Rameah  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Vernet, Corine A.  
; APPLICANT: Li, Li  
; APPLICANT: Gorman, Linda  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Taupier, Raymond J., Jr.  
; APPLICANT: Miller, Charles  
; APPLICANT: Casman, Stacie  
; APPLICANT: Pena, Carol  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Gusev, Vladimir

```

; APPLICANT: Smithson, Glennda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Gerlach, Valerie
; APPLICANT: Fochart, Pascal
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: LaRocheille, William
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-290 B
; CURRENT APPLICATION NUMBER: US/10/094,886
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,182
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/288,052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314,018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296,693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313,626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 115
; LENGTH: 2898
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21)..(2871)
US-10-094-886-115

Query Match      82.6%; Score 2260; DB 17; Length 2898;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 2562; Conservative 0; Mismatches 25; Indels 237; Gaps 5;

QY 102 AGGAACGTGACAAATGGCGAAGCCCTTCCGGAATCCATCCATCAGCTCCCTGGGACACTGCC 161
DB 98 AGGAACGTGACAAATGGCGAAGCCCTTCCGGAATCCATCCATCAGCTCCCTGGGACACTGCC 157
QY 162 TCATTTTCATAGAGAGCAGATGATGCTTATATATCAAGAGCAACCTATTGCACTCAG 221
DB 158 TCATTTTCATAGAGAGCAGATGATGCTTATATATCAAGAGCAACCTATTGCACTCAG 217
QY 222 GTGCAAGAGCAGGCGAGCAGATGATGCTTATATCAAGAGCAACCTATTGCACTCAG 281
DB 218 GTGCAAGAGCAGGCGAGCAGATGATGCTTATATCAAGAGCAACCTATTGCACTCAG 277
QY 282 GAACGAGCAGCTCTCTGAAGAGACTCTGGAGAGAGCTCAGAGTCTTGAAGTCCGCGAAGT 341
DB 278 GAACGAGCAGCTCTCTGAAGAGACTCTGGAGAGAGCTCAGAGTCTTGAAGTCCGCGAAGT 337
QY 342 GTTCATCAATGTTTACTAGGCAACAGGTGGAGGACTTCCATGGGCGCGAGGACTATTGGTG 401
DB 338 GTTCATCAATGTTTACTAGGCAACAGGTGGAGGACTTCCATGGGCGCGAGGACTATTGGTG 397
QY 402 CCAGTGTGGCGTGGAGCCACCTGGGTACTTCCAGAGCAGAGAGCCCTCTGTGGGCAT 461
DB 398 CCAGTGTGGCGTGGAGCCACCTGGGTACTTCCAGAGCAGAGAGCCCTCTGTGGGCAT 457

```

```

QY 462 AGCCTATTATCGGAAAACTTTGAACAAGAACCCCAAGAGGGAAGTTCCCATTTGAAGG 521
DB 458 AGCCTATTATCGGAAAACTTTGAACAAGAACCCCAAGAGGGAAGTTCCCATTTGAAGG 517
QY 522 CATGATTGTACTGCTCGCGCCACCAAGAGGAGTCCCTGCTGCGAGGTGGAATGGCT 581
DB 518 CATGATTGTACTGCTCGCGCCACCAAGAGGAGTCCCTGCTGCGAGGTGGAATGGCT 577
QY 582 GAARAATGAAGAGCCCATTTGACTCTGAAACAAGACGAGAACATTGACACACAGGCTTGACCA 641
DB 578 GAARAATGAAGAGCCCATTTGACTCTGAAACAAGACGAGAACATTGACACACAGGCTTGACCA 637
QY 642 TAACTCTGATCATCAGGCGAGGCAAGCTCTCGGACTCAGGAAATTAACCTGTCATGGCAGC 701
DB 638 TAACTCTGATCATCAGGCGAGGCAAGCTCTCGGACTCAGGAAATTAACCTGTCATGGCAGC 697
QY 702 CAAATCTGGCTTAAGAGAGAGAGCTCTGCGGCACTGTTGGTCTTAC----- 750
DB 698 CAAATCTGGCTTAAGAGAGAGAGCTCTGCGGCACTGTTGGTCTTAC----- 757
QY 751 ----- 750
DB 758 CTGGTCTCTCTGGACAGAGTGGTCAAGCTGCTGCTGCTGGTAGAGATGCGAGAA 817
QY 751 ----- 750
DB 818 ACGTTTCCGGACCTGCACCAACCCAGCTCTCTCAATGGTGGGCGCTTTTGTGAGGGAAT 877
QY 751 -----GTGGATGGAGCTGGGAGTGG 773
DB 878 GTGAGTGCAAGAAATAAACCCTGCATCTCTTTGTCTCTGTGGATGGAGCTGGGAGTGG 937
QY 774 GAGCGAATGGTCCGCTCTGCAGTCCAGAGTGTCAACATTTGCGGATCCCGGAGTGCACAGC 833
DB 938 GAGCGAATGGTCCGCTCTGCAGTCCAGAGTGTCAACATTTGCGGATCCCGGAGTGCACAGC 997
QY 834 ACCACCCCGAGAAATGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAAATCTGAAACCTG 893
DB 998 ACCACCCCGAGAAATGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAAATCTGAAACCTG 1057
QY 894 CACAGATGGTCTTTGCTGCTAGATAAATAAAGCTCTTCAATGAATAATAAATCCCAAGC-- 951
DB 1058 CACAGATGGTCTTTGCTGCTAGATAAATAAAGCTCTTCAATGAATAATAAATCCCAAGC-- 1117
QY 952 -----ATTGAGAAATGCCAGCAGACATTTGCTTTGTACTCGGGCTTGGGTGC 995
DB 1118 TCAGAGCGCTATGCCAAATTTGAGATGCCAGCGACATTTGTTGTACTCGGGCTTGGGTGC 1177
QY 996 TGCCTGTGCGGCGTGTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055
DB 1178 TGCCTGTGCGGCGTGTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1237
QY 1056 TGACTATGCGGTGGAGCTCATTTGACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1115
DB 1238 TGACTATGCGGTGGAGCTCATTTGACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1297
QY 1116 CTTTAAAAACAGTCCGCTCAAGCAAGAAATATCATGGAATTAATGATAAAGAAATTCCTT 1175
DB 1298 CTTTAAAAACAGTCCGCTCAAGCAAGAAATATCATGGAATTAATGATAAAGAAATTCCTT 1316
QY 1176 TGTGTAATCTCCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1235
DB 1317 -GGGAATCTCCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1375
QY 1236 CAGCGAGCCCATCTGCTGCGAGCCCTCTGGAACAGAGAGCTCATGACAGAGTCTTCACT 1295
DB 1376 CAGCGAGCCCATCTGCTGCGAGCCCTCTGGAACAGAGAGCTCATGACAGAGTCTTCACT 1435
QY 1296 CTTTAAACCCCTTTGTGCGGACATCAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGG 1355
DB 1436 CTTTAAACCCCTTTGTGCGGACATCAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGG 1495

```

QY 1356 AGTGTCTGAGAGCTGAGTACCAACGCGAAGATCATTCAGGACTTTTCCCATGGAAA 1415  
Db 1496 AGTGTCTGAGAGCTGAGTACCAACGCGAAGATCATTCAGGACTTTTCCCATGGAAA 1555  
QY 1416 CAACACAGCTTTAGTACAAATGATCCAGAAATAAAATCCCTTACATCCAAATCTGTC 1475  
Db 1556 CAACACAGCTTTAGTACAAATGATCCAGAAATAAAATGCTTACATCCAAATCTGTC 1515  
QY 1476 ATCACTCCCAAGGACAGAACTGAGGACAACTGTGTCTTTGGGCATTTAGGGGGGG 1535  
Db 1616 ATCACTCCCAAGGACAGAACTGAGGACAACTGTGTCTTTGGGCATTTAGGGGGGG 1675  
QY 1536 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTATACACACAGGTGCCATCCAGGGA 1595  
Db 1676 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTATACACACAGGTGCCATCCAGGGA 1735  
QY 1596 GAATTTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCTCCAGTCAAGTGG 1655  
Db 1736 GAATTTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG-----GTCAAGTGG 1789  
QY 1656 CTCTGAGGTGCTCTGAGTCTGAGTCACTGTGTGTCTTCCAGAGATGATGTCACCC 1715  
Db 1790 CTCTGAGGTGCTCTGAGTCTGAGTCACTGTGTGTCTTCCAGAGATGATGTCACCC 1849  
QY 1716 TCCCTTTGCAATGACCATCCGCACTGTGCAGATGTCAGTCTGAGCATTTGGATATCCA 1775  
Db 1850 TCCCTTTGCAATGACCATCCGCACTGTGCAGATGTCAGTCTGAGCATTTGGATATCCA 1909  
QY 1776 TTTAAAGAGAGACACAGCAGGCGCAATGGGAGGAAGTATGTCAGTGGAAATGAATC 1835  
Db 1910 TTTAAAGAGAGACACAGCAGGCGCAATGGGAGGAAGTATGTCAGTGGAAATGAATC 1969  
QY 1836 TACATCTGTATCTGCTTTTGGACCCCTTTGGTGTGTCATGTCTCTGAGACAGCTTTGG 1895  
Db 1970 TACATCTGTATCTGCTTTTGGACCCCTTTGGTGTGTCATGTCTCTGAGACAGCTTTGG 2029  
QY 1896 GACCTATGCTCACTGGAGGCAATCAAGAGTGTGCGGTGAAGCACTGAAGTGGC 1955  
Db 2030 GACCTATGCTCACTGGAGGCAATCAAGAGTGTGCGGTGAAGCACTGAAGTGGC 2089  
QY 1956 GGTTTTGGCTGATGCTCTGTAACCTCCCTGGATTAACATTCAGAGATTTACTGTGGA 2015  
Db 2090 GGTTTTGGCTGATGCTCTGTAACCTCCCTGGATTAACATTCAGAGATTTACTGTGGA 2149  
QY 2016 CAATACCCCTTGTGCAATTCAGGAAGTGTGTTTCAAGTAAAGGCATCAAGGTGGAAGCT 2075  
Db 2150 CAATACCCCTTGTGCAATTCAGGAAGTGTGTTTCAAGTAAAGGCATCAAGGTGGAAGCT 2209  
QY 2076 CCTGGAAGAACCAAAATTTGCTGATTTCAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2135  
Db 2210 CCTGGAAGAACCAAAATTTGCTGATTTCAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2269  
QY 2136 CCTTGATATTCCTCCCATCTCTGGAGATTTAAACCAATTCACCTGCTGCCAGGAAGTCCC 2195  
Db 2270 CCTTGATATTCCTCCCATCTCTGGAGATTTAAACCAATTCACCTGCTGCCAGGAAGTCCC 2329  
QY 2196 GTTCTCCCGGTGTGTGCAATTAACCGGAGCCCTTGCATGTGCTCTTCCCTGGAGCG 2255  
Db 2330 GTTCTCCCGGTGTGTGCAATTAACCGGAGCCCTTGCATGTGCTCTTCCCTGGAGCG 2389  
QY 2256 TTATAGCCCACTACCAACCCAGCTGTCTGCAAAATCTGCAATTCGGAGCTCAAGGCCA 2315  
Db 2390 TTATAGCCCACTACCAACCCAGCTGTCTGCAAAATCTGCAATTCGGAGCTCAAGGCCA 2449  
QY 2316 TGAACAGATCTCCAAAGTGAGACATCAATCTCTAGAGAGTGAACGAGAAACCACTACTTT 2375  
Db 2450 TGAACAGATCTCCAAAGTGAGACATCAATCTCTAGAGAGTGAACGAGAAACCACTACTTT 2509  
QY 2376 CTTTCGACAAAGAGGACAGCACTTTTCCCTGCAAGACTGGCCCCCAAGCCCTTCAAAATTC 2435  
Db 2510 CTTTCGACAAAGAGGACAGCACTTTTCCCTGCAAGACTGGCCCCCAAGCCCTTCAAAATTC 2569  
QY 2436 CTACTCCATCAGACAGGGGATTTGTGCTACATTTGTATACCCCAATGCCAAAGGCAAGGA 2495

Db 2570 CTACTCCATCAGACAGCGGATTTGTCTACATTTGATACCCCAATGCCAAAGGCAAGGA 2629  
QY 2496 CTGGCAGATGTTAGCACAGAAAAACAGCATCAAC---AGGAATTTATCTTTATTTGCTAC 2552  
Db 2630 CTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAGGAATTTATCTTTGCTAC 2689  
QY 2553 ACAAGTAGCCCATCTGCTGTCTATTTTGAACCTGTGGGAAGCTGCTCATCAGCATGATGG 2612  
Db 2690 ACAAGTAGCCCATCTGCTGTCTATTTTGAACCTGTGGGAAGCTGCTCATCAGCATGATGG 2749  
QY 2613 TGATCTTTGACTCCCTGGCCCTGTGCTTGAAGAGATTTGGGAGGACACACAGCAAACTCTC 2672  
Db 2750 TGATCTTTGACTCCCTGGCCCTGTGCTTGAAGAGATTTGGGAGGACACACAGCAAACTCTC 2809  
QY 2673 AAACATTTCAGAAATCCAGCTTGATGAAGCCGACTTTCAACTACAGCAGGCAAAATGGACT 2732  
Db 2810 AAACATTTCAGAAATCCAGCTTGATGAAGCCGACTTTCAACTACAGCAGGCAAAATGGACT 2869  
QY 2733 CTAG 2736  
Db 2870 CTAG 2873

RESULT 10  
US-10-872-681-53  
; Sequence 53, Application US/10872681  
; Publication No. US20050026251A1  
; GENERAL INFORMATION:  
; APPLICANT: ARES TRADING LIMITED  
; TITLE OF INVENTION: TRANSMEMBRANE PROTEIN  
; FILE REFERENCE: P029209NO  
; CURRENT APPLICATION NUMBER: US/10/872,681  
; CURRENT FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: GB0130721.4  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: SeqWin99, version 1.02  
; SEQ ID NO 53  
; LENGTH: 2661  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SEQ ID NO:31  
US-10-872-681-53

Query Match 81.1%; Score 2220; DB 19; Length 2661;  
Best Local Similarity 91.1%; Pred. No. 0;  
Matches 2493; Conservative 0; Mismatches 0; Indels 243; Gaps 3;

QY 124 CTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCTCATTTATAGAGGCCAGAT 183  
Db 1 CTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCTCATTTATAGAGGCCAGAT 60  
QY 184 GATGCTTATATTATCAAGAGCAACCTTATTCAGTTCAGGTGCAAGCGGCCAGCCATG 243  
Db 61 GATGCTTATATTATCAAGAGCAACCTTATTCAGTTCAGGTGCAAGCGGCCAGCCATG 120  
QY 244 CAGATATTCTTCAAAATGCAACGCGAGTGGTCCATCAGAAACGAGACGCTCTCTGAAGAG 303  
Db 121 CAGATATTCTTCAAAATGCAACGCGAGTGGTCCATCAGAAACGAGACGCTCTCTGAAGAG 180  
QY 304 ACTCTGGACGAGGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGGCAA 363  
Db 181 ACTCTGGACGAGGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGGCAA 240  
QY 364 CAGGTGGAGGACTTCCATGGGCCGAGGACTATTGTCGAGTGTGTGGCGTGGAGCCAC 423  
Db 241 CAGGTGGAGGACTTCCATGGGCCGAGGACTATTGTCGAGTGTGTGGCGTGGAGCCAC 300  
QY 424 CTGGGTACCTCCAAAGAGCAGGAGGCTCTGTGCGCATAGCTTATTTACGGAACAACTTT 483  
Db 301 CTGGGTACCTCCAAAGAGCAGGAGGCTCTGTGCGCATAGCTTATTTACGGAACAACTTT 360







[illegible]

RESULT 11  
US-10-798-721-25  
; Sequence 25, Application US/10798721  
; Publication No. US20040248166A1  
; GENERAL INFORMATION:  
; APPLICANT: Walke, D. Wade  
; APPLICANT: Scoville, John  
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the Same

```

; CUREN RE-APPLICATIO: USR 0213 008
; CURRENT APPLICATION NUMBER: US/10/798,721
;
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
;
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-721-25

```

Query Match	74.7%	Score 2043;	DB 18;	Length 2043;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2043;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

694	ATGGCAGCCAAACATCGTGGCTAAGAGAGAAGCCTGTGCGGCACCTGTTGTGCTACGTG	753
Qy		
1	ATGGCAGCCAAACATCGTGGCTAAGAGAGAAGCCTGTGCGGCACCTGTTGTGCTACGTG	60
Db		
754	GATGGGAGCTGGGAAGTGTGGAGCGAATGTCGCTCTGCAGTCCAGAGTGTGAACATTG	813
Qy		
61	GATGGGAGCTGGGAAGTGTGGAGCGAATGTCGCTCTGCAGTCCAGAGTGTGAACATTG	120
Db		
814	CGGATCCGGAGTGCACAGCACACACCCCGAGAAATGGGGGCAAAATCTGTGAAGGCTTA	873
Qy		
121	CGGATCCGGAGTGCACAGCACACCCCGAGAAATGGGGGCAAAATCTGTGAAGGCTTA	180
Db		
874	AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGTCATCCTAGATAAAAAACCTCTTCAT	933
Qy		
181	AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGTCATCCTAGATAAAAAACCTCTTCAT	240
Db		
934	GAATAAACCCTGAAAGCATTTGAGATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT	993
Qy		
241	GAATAAACCCTGAAAGCATTTGAGATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT	300
Db		
994	GCTGCGCTGCTGCGCGTTGCAGTCTCGTCAATGGTGTCACTCCCTTTACAGACGGAGCCAG	1053
Qy		
301	GCTGCGCTGCTGCGCGTTGCAGTCTCGTCAATGGTGTCACTCCCTTTACAGACGGAGCCAG	360
Db		
1054	AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCAATGACAGGTGGCTTCCAGACCTTC	1113
Qy		
361	AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCAATGACAGGTGGCTTCCAGACCTTC	420
Db		
1114	AACCTTCAAAACAGTCCGCTCAAGCCAGAATACTATGGAACCTAATGATACAAGAAAAATCC	1173
Qy		

421	Db	AACTTCAAAACAGCTCGGTCAAGCCCAAGATATCATATGGAATCAATATGATATACAAGAAAAATCC	480
1174	Qy	TTTGGTAAATCCCTGCTCCTGGAATTTCTGCCATGCAGCCAGATCTGAAGAGTGGCGGACA	1233
481	Db	TTTGGTAACTCCCTGCTCCTGGAATTTCTGCCATGCAGCCAGATCTGAAGAGTGGCGGACA	540
1234	Qy	TACAGCGGACCAATCTGTCTGTGAGGACCTCTCTGGACAAGAGAGTCTATGACAGAGTCTCTCA	1293
541	Db	TACAGCGGACCAATCTGTCTGTGAGGACCTCTCTGGACAAGAGAGTCTATGACAGAGTCTCTCA	600
1294	Qy	CTCTTTAAACCTTTGTCTGGACATCAAAGTGAAAGTCCAGAGCTCGTTCTATGTTTCCCTG	1353
601	Db	CTCTTTAAACCTTTGTCTGGACATCAAAGTGAAAGTCCAGAGCTCGTTCTATGTTTCCCTG	660
1354	Qy	GGAGTCTGTGAGAGAGCTGAGTACACCGGCAAGAAATCATTTCCAGGACTTTTCCCATGGA	1413
661	Db	GGAGTCTGTGAGAGAGCTGAGTACACCGGCAAGAAATCATTTCCAGGACTTTTCCCATGGA	720
1414	Qy	AACAACACAGCTTTTAGTACAATGCAATCCAGAAAAATAAATAGCCCTACATCCAAAATCTG	1473
721	Db	AACAACACAGCTTTTAGTACAATGCAATCCAGAAAAATAAATAGCCCTACATCCAAAATCTG	780
1474	Qy	TCATCACTCCCCACAAGGACAGAACTGAGACAACTGGTGCTCTTTGGCCATTTAGGGGGG	1533
781	Db	TCATCACTCCCCACAAGGACAGAACTGAGACAACTGGTGCTCTTTGGCCATTTAGGGGGG	840
1534	Qy	CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACACACGGTGCCATCCACAG	1593
841	Db	CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACACACGGTGCCATCCACAG	900
1594	Qy	GAGAAATCTTGGAGATTTATATGTGCATCAACCAAGGTGAACCCAGCTCCAGTCAAGT	1653
901	Db	GAGAAATCTTGGAGATTTATATGTGCATCAACCAAGGTGAACCCAGCTCCAGTCAAGT	960
1654	Qy	GGCTCTGAGGTGCTCTGTGCTCTGAGTCACTGAGTCACTGCTGGTCTCTCCAGACATGATCGTCACC	1713
961	Db	GGCTCTGAGGTGCTCTGTGCTCTGAGTCACTGAGTCACTGCTGGTCTCTCCAGACATGATCGTCACC	1020
1714	Qy	ACTCCCTTTGCATTTGACCATCCCGCACTGTGCAGATGTCTAGTTCTTGAGCATTTGGAATATC	1773
1021	Db	ACTCCCTTTGCATTTGACCATCCCGCACTGTGCAGATGTCTAGTTCTTGAGCATTTGGAATATC	1080
1774	Qy	CATTTAAAGAGGACACACAGCAGGGCAAAATGGAGGAAGTGAATGTCAAGTGGAAAGATGAA	1833
1081	Db	CATTTAAAGAGGACACACAGCAGGGCAAAATGGAGGAAGTGAATGTCAAGTGGAAAGATGAA	1140
1834	Qy	TCTACATCTGTTTACTGTCCTTTTGGACCCCTTTTGGTGTGATGTGCTCTCTGGACAGCTTT	1893
1141	Db	TCTACATCTGTTTACTGTCCTTTTGGACCCCTTTTGGTGTGATGTGCTCTCTGGACAGCTTT	1200
1894	Qy	GGACCTATCGCTCTACTGGAGAGCCAAATCACAGACTGTGCGGTGAAGCAACTGAAGGTG	1953
1201	Db	GGACCTATCGCTCTACTGGAGAGCCAAATCACAGACTGTGCGGTGAAGCAACTGAAGGTG	1260
1954	Qy	CGGGTTTTGGCTGCAATGCTCTGTAACTCCCTGGAATTAACAATGAGAGTTTACTGTGTG	2013
1261	Db	CGGGTTTTGGCTGCAATGCTCTGTAACTCCCTGGAATTAACAATGAGAGTTTACTGTGTG	1320
2014	Qy	GACAAATCCCTTTGTGCATTTTCAGGAAGTGGTTTCAGATGAAGGCATCAAGGTGGACAG	2073
1321	Db	GACAAATCCCTTTGTGCATTTTCAGGAAGTGGTTTCAGATGAAGGCATCAAGGTGGACAG	1380
2074	Qy	CTCTGGAAGAACCAAAATTTGCTGCATTTTCAAAGGGAATACCTTTTAGTCTTTCAGATTTCT	2133
1381	Db	CTCTGGAAGAACCAAAATTTGCTGCATTTTCAAAGGGAATACCTTTTAGTCTTTCAGATTTCT	1440
2134	Qy	GTCTTTGATATCCCCCATTTCTCTGAGAGAAATAAACCAATTTCACTGCTGTCAGGAAGTC	2193
1441	Db	GTCTTTGATATCCCCCATTTCTCTGAGAGAAATAAACCAATTTCACTGCTGTCAGGAAGTC	1500
2194	Qy	CCGTTCTCCCGGTGGTGCAGTAAACCGGAGCCCTCTGCACTGTGCTTCTCCCTGGAG	2253
1501	Db	CCGTTCTCCCGGTGGTGCAGTAAACCGGAGCCCTCTGCACTGTGCTTCTCCCTGGAG	1560



Db	1168	GGGACCTATCGCTCATCTGGAGAGCCAAATCACAGACTGTCCGTGAAGCAACTGAAGGTG	1227
Qy	1954	CGCGTTTTTGGCTGCGATGTCCTGTAACTCCCTGGATTACAACCTTGAGAGTTTACTGTGTG	2013
Db	1228	CGCGTTTTTGGCTGCGATGTCCTGTAACTCCCTGGATTACAACCTTGAGAGTTTACTGTGTG	1287
Qy	2014	GACAATACCCCTTGTGTGATTTTCAGGAAGTGGTTTTAGATGAAGGCATCAAGGTGGACAG	2073
Db	1288	GACAATACCCCTTGTGTGATTTTCAGGAAGTGGTTTTAGATGAAGGCATCAAGGTGGACAG	1347
Qy	2074	CTCTGGAAGAACCAAAATTTCTGCAATTTCAAGGGGAATACCTTTAGTCTTTCAGATTTCT	2133
Db	1348	CTCTGGAAGAACCAAAATTTCTGCAATTTCAAGGGGAATACCTTTAGTCTTTCAGATTTCT	1407
Qy	2134	GTCCTTGATATTCCTCCCATTTCTCTGAGAAATTAACCATTTCACTGCTGCCAGGAAGTC	2193
Db	1408	GTCCTTGATATTCCTCCCATTTCTCTGAGAAATTAACCATTTCACTGCTGCCAGGAAGTC	1467
Qy	2194	CGGTTCTCCCGGTGTGGTGAGTAACCGGGAGCCCTGTGACTGTGTGCTTCTCCCTGGAG	2253
Db	1468	CGGTTCTCCCGGTGTGGTGAGTAACCGGGAGCCCTGTGACTGTGTGCTTCTCCCTGGAG	1527
Qy	2254	CGTTATACGCCCACTACACCCAGCTGCTCTGCAGAAATCTGCATTCGGCAGCTCAAGGC	2313
Db	1528	CGTTATACGCCCACTACACCCAGCTGCTCTGCAGAAATCTGCATTCGGCAGCTCAAGGC	1587
Qy	2314	CATGAACAGATCTCTCAAAGTCGACACATCAATCCTAGAGAGTGAAACGAGAAACCATCACT	2373
Db	1588	CATGAACAGATCTCTCAAAGTCGACACATCAATCCTAGAGAGTGAAACGAGAAACCATCACT	1647
Qy	2374	TTCTTCGCAACAGAGGACAGACATTTTCCCTGCGACAGACTGGCCCCCAAGCCTTCAAAAT	2433
Db	1648	TTCTTCGCAACAGAGGACAGACATTTTCCCTGCGACAGACTGGCCCCCAAGCCTTCAAAAT	1707
Qy	2434	CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATATCCCCCATGCCAAGGCAAG	2493
Db	1708	CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATATCCCCCATGCCAAGGCAAG	1767
Qy	2494	GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTTCGCTACA	2553
Db	1768	GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTTCGCTACA	1827
Qy	2554	CAAAAGTAGCCCATCTGCTGTCAATTTTGAACCTGTGGGAAGCTGCTCATCAGCATGATGGT	2613
Db	1828	CAAAAGTAGCCCATCTGCTGTCAATTTTGAACCTGTGGGAAGCTGCTCATCAGCATGATGGT	1887
Qy	2614	GATCTTCACCTCCCTGGCTGTGCCCTTGAAGAGATTCGGGAGGACACACAGAACTCTCA	2673
Db	1888	GATCTTCACCTCCCTGGCTGTGCCCTTGAAGAGATTCGGGAGGACACACAGAACTCTCA	1947
Qy	2674	AACATTTTCAGAAATCCCAAGCTTGATGAAGCCGACTTCAACTACAGACGCAAAATGGACTC	2733
Db	1948	AACATTTTCAGAAATCCCAAGCTTGATGAAGCCGACTTCAACTACAGACGCAAAATGGACTC	2793
Qy	2734	TAG 2736	
Db	2008	TAG 2010	

RESULT 13

```

RESD01.13
US-10-798-721-29
; Sequence 29, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/10/798,721
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02

```

QY	1594	GAGAAATTCCTTGGGAGATTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCCAGAT	1653
Db	859	GAGAAATTCCTTGGGAGATTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCCAGAT	918
QY	1654	GGCTCTGAGGTGCTCCTGAGTCCCTGAAGTCAACCTGTGCTCTCCAGACATGATCGTCACC	1713
Db	919	GGCTCTGAGGTGCTCCTGAGTCCCTGAAGTCAACCTGTGCTCTCCAGACATGATCGTCACC	978
QY	1714	ACTCCCTTTGCAATTGACCATCCCGCACTGTGCAGATGTCAAGTTCTGAGCAATTGGAAATATC	1773
Db	979	ACTCCCTTTGCAATTGACCATCCCGCACTGTGCAGATGTCAAGTTCTGAGCAATTGGAAATATC	1038
QY	1774	CATTTAAGAAGAGGACACACGACGGGCAAAATGGAGGAAGTGAATGTCAAGTGGAAAGATGAA	1833
Db	1039	CATTTAAGAAGAGGACACACGACGGGCAAAATGGAGGAAGTGAATGTCAAGTGGAAAGATGAA	1098
QY	1834	TCTACATCTCGTTACTGCTTTTGACCCCTTTTGCAGCCCTTTCGCTGATGTGCTCTCGGACAGCTTT	1893
Db	1099	TCTACATCTCGTTACTGCTTTTGACCCCTTTCGCTGATGTGCTCTCGGACAGCTTT	1158
QY	1894	GGGACCTATGCGCTCAGCTGGAGAGCCCAATCACAGACTGTGCCGTGAAGCAACTGGAAGGTG	1953
Db	1159	GGGACCTATGCGCTCAGCTGGAGAGCCCAATCACAGACTGTGCCGTGAAGCAACTGGAAGGTG	1218
QY	1954	CGCGTTTTTGGCTCGATGTCTCTGTAACTCCCTGTGAATTAACAATTGAGAGTTTACTGHTGTG	2013
Db	1219	CGCGTTTTTGGCTCGATGTCTCTGTAACTCCCTGTGAATTAACAATTGAGAGTTTACTGHTGTG	1278
QY	2014	GACAATACCCCTGTGTGCAATTTACAGAAAGTGTGTTTCAGATGAAAGGCATCAAGGTGGACAG	2073
Db	1279	GACAATACCCCTGTGTGCAATTTACAGAAAGTGTGTTTCAGATGAAAGGCATCAAGGTGGACAG	1338
QY	2074	CTCCTGGAAGAACCAAAATTTGCTGCATTTCAAAGGGAATACCTTTAGCTTTCAGATTTCT	2133
Db	1339	CTCCTGGAAGAACCAAAATTTGCTGCATTTCAAAGGGAATACCTTTAGCTTTCAGATTTCT	1398
QY	2134	GTCCCTGATATTTCCGCCATTTCTCTGGAGAAATTAACCAATTCAGTGCCTGCCAGGAATC	2193
Db	1399	GTCCCTGATATTTCCGCCATTTCTCTGGAGAAATTAACCAATTCAGTGCCTGCCAGGAATC	1458
QY	2194	CCGTTCTCCCGCGTGTGTGCAGTAAACCGGCAGCCCTGCACTGTGTGCTTTCTCCCTGGAG	2253
Db	1459	CCGTTCTCCCGCGTGTGTGCAGTAAACCGGCAGCCCTGCACTGTGTGCTTTCTCCCTGGAG	1518
QY	2254	CGTTATAGCCCACTACACCCAGCTGTCTGCMAAAATCTGCAATTCGGCAGCTCAAAGGC	2313
Db	1519	CGTTATAGCCCACTACACCCAGCTGTCTGCMAAAATCTGCAATTCGGCAGCTCAAAGGC	1578
QY	2314	CATGAAACAGATCCTTCAAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT	2373
Db	1579	CATGAAACAGATCCTTCAAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT	1638
QY	2374	TTCTTTCGCAACAAGGAGCAGCACTTTCCCTGCAAGACTGGCCCCCAAGGCTTTCAAATTT	2433
Db	1639	TTCTTTCGCAACAAGGAGCAGCACTTTCCCTGCAAGACTGGCCCCCAAGGCTTTCAAATTT	1698
QY	2434	CCCTACTCCATCAGACAGGGATTTTGTGCTACATTTGATACCCGCCAATGCCAAGGCAAG	2493
Db	1699	CCCTACTCCATCAGACAGGGATTTTGTGCTACATTTGATACCCGCCAATGCCAAGGCAAG	1758
QY	2494	GACTGGCAGATGTTTGGACAGAAAAACAGCATCAACAGGAATTTATCTTATTTTCGCTACA	2553
Db	1759	GACTGGCAGATGTTTGGACAGAAAAACAGCATCAACAGGAATTTATCTTATTTTCGCTACA	1818
QY	2554	CAAAAGTAGCCCATCTGCTGTCAATTTTGAAACCTGTGGGAAGCTCGTCATCAGCATGTATGTT	2613
Db	1819	CAAAAGTAGCCCATCTGCTGTCAATTTTGAAACCTGTGGGAAGCTCGTCATCAGCATGTATGTT	1878
QY	2614	GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTTGGGAGGACACACAGAAAATCTCTCA	2673
Db	1879	GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTTGGGAGGACACACAGAAAATCTCTCA	1938

```

Qy      2674 AACATTTTCAGAAATCCCGACGCTTGATGAAGCCGCACTTCAACTACAGCAGCGCAAATGGACTC. 2733
          |||||
Db      1939 AACATTTTCAGAAATCCCGACGCTTGATGAAGCCGCACTTCAACTACAGCAGCGCAAATGGACTC
          |||||
Qy      2734 TAG 2736
          |||
Db      1999 TAG 2001
          |||

RESULT 14
US-10-798-721-31
; Sequence 31, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/10798,721
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-721-31

```

	Query Match	68.5%; Score 1873; DB 18; Length 1968;
	Best Local Similarity	96.3%; Pred. No. 0;
	Matches 1968; Conservative	0; Mismatches 0; Indels 75; Gaps 2;
Qy	694	ATGCGCACCACATCGTGGCTAAAGAGAGAGAGCGCTGTCCGCCACTGTGTGGTCTACGTG 753
Dd	1	ATGCGCACCACATCGTGGCTAAAGAGAGAGCGCTGTCCGCCACTGTGTGGTCTACGTG 60
Qy	754	GATGGGAGCTGGGAAGTGTCGAGCGAATGGTCGGTCTGCAGTCCAGAGTGTGAACATTGTG 813
Dd	61	GATGGGAGCTGGGAAGTGTCGAGCGAATGCTCCGTCTGCAGTCCAGAGTGTGAACATTGTG 126
Qy	814	CGGATCCGGAGTGTCAAGCACACACCCCCAGAAAATGGGGGCAAATCTCTGAAGTCTA 873
Dd	121	CGGATCCGGAGTGTCAAGCACACACCCCCAGAAAATGGGGGCAAATCTCTGAAGTCTA 180
Qy	874	AGCCAGGAATCTGAAACTGCACAGATGGTCTTTGCACTCTAGATAAAAAACCTCTTCAT 933
Dd	181	AGCCAGGAATCTGAAACTGCACAGATGGTCTTTGCACTCTAGATAAAAAACCTCTTCAT 223
Qy	934	GAATAAAACCCCAAAGCATTTGAGAATGCCAGCGACAATGCTTTTGTACTCGGGCTTGGGT 993
Dd	224	-----GCAATTGAGAATGCCAGCGACAATGCTTTTGTACTCGGGCTTGGGT 267
Qy	994	GCTGCCGTCTGGCCGTGTGACGTCCTGGTCAATTTGGTGTACCCCTTTACAGACGGAGCCAG 1053
Dd	268	GCTGCCGTCTGGCCGTGTGACGTCCTGGTCAATTTGGTGTACCCCTTTACAGACGGAGCCAG 327
Qy	1054	AGTGACTATCGCGTGGACGTCATTGTACTCTTCGTCAATTGACAGGTGGCTTCCAGACCTTC 1113
Dd	328	AGTGACTATCGCGTGGACGTCATTGTACTCTTCGTCAATTGACAGGTGGCTTCCAGACCTTC 387
Qy	1114	AAC TTC AAAAACAGTCCCGTCAAGCCAAAGAAATATCATGGAACTAATGATACAGAAAAATCC 1173
Dd	388	AAC TTC AAAAACAGTCCCGTCAA----- 408
Qy	1174	TTTTGGTAACCTCCCTGCTCTGAATTCGCCATCGACGCCAGATCTGACAGTGAAGCCGACA 1233
Dd	409	----GGTAAC TCCCTGTCTCTGAATTCGCCATCGACGCCAGATCTGACAGTGAAGCCGACA 465
Qy	1234	TACAGCGGAGCCCATCTGTCTGCGAGGACCCCTCTCGGACAAAGAGAGTCTATGACAGAGTCCCTCA 1293

```
|||||
466 TACAGCGGACCCATCTGTCTGCGAGGACCTCTGTGCAAGAGGCTCATGACAGAGTCTCTCA 525
QY
1294 CTCTTTAAACCTTTGTGCGGACATCAAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTG 1353
Db
526 CTCTTTAAACCTTTGTGCGGACATCAAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTG 585
QY
1354 GAGTGTCTGAGAGAGCTGAGTACCACCGGCAAGATCAATTCAGGACTTTTCCCATGGA 1413
Db
586 GAGTGTCTGAGAGAGCTGAGTACCACCGGCAAGATCAATTCAGGACTTTTCCCATGGA 645
QY
1414 AACACACACAGCTTTAGTACAAATGTCATCCAGAGAAATAAATGCGCTACATCCCAAATCTG 1473
Db
646 AACACACACAGCTTTAGTACAAATGTCATCCAGAGAAATAAATGCGCTACATCCCAAATCTG 705
QY
1474 TCATCACTCCCAACAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGG 1533
Db
706 TCATCACTCCCAACAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGG 765
QY
1534 CGCTTAGTAATGCCAATACAGGGGTGAGCTTACTATACACACGCGTCCCATCCAGAG 1593
Db
766 CGCTTAGTAATGCCAATACAGGGGTGAGCTTACTATACACACGCGTCCCATCCAGAG 825
QY
1594 GAGAAATCTTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAAGT 1653
Db
826 GAGAAATCTTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAAGT 885
QY
1654 GGCTCTGAGGTGCTCTGAGTCTCTGAAAGTCACTGTGTCTCCAGACATGATCGTCACC 1713
Db
886 GGCTCTGAGGTGCTCTGAGTCTCTGAAAGTCACTGTGTCTCCAGACATGATCGTCACC 945
QY
1714 ACTCCCTTTGCATTGACCATCCGCACTGCGAGATGTCAGATGTCAGAGATTTGGAATATC 1773
Db
946 ACTCCCTTTGCATTGACCATCCGCACTGCGAGATGTCAGATGTCAGAGATTTGGAATATC 1805
QY
1774 CATTTAAAGAGAGGACACAGAGGCAATGGAGGAAGTGTGTCAGTGGAGAGATGAA 1833
Db
1806 CATTTAAAGAGAGGACACAGAGGCAATGGAGGAAGTGTGTCAGTGGAGAGATGAA 1865
QY
1834 TCTACATCTCTGTACTGCTCTTTTGGACCCCTTTGCGTGTGTCATGTCTCTGGACAGCTTT 1893
Db
1866 TCTACATCTCTGTACTGCTCTTTTGGACCCCTTTGCGTGTGTCATGTCTCTGGACAGCTTT 1925
QY
1894 GGGACCTATCGCTCTACTGAGAGGCAATACAGACTGTGCGTGAAGCAACTGAAGGTG 1953
Db
1126 GGGACCTATCGCTCTACTGAGAGGCAATACAGACTGTGCGTGAAGCAACTGAAGGTG 1185
QY
1954 GCGGTTTTTGGCTGCACTGCTGTAACCTCCCTGATTTACAACTTGAGAGTTTACTGTGTG 2013
Db
1186 GCGGTTTTTGGCTGCACTGCTGTAACCTCCCTGATTTACAACTTGAGAGTTTACTGTGTG 1245
QY
2014 GACAATAACCCCTTTGTGATTTTCAAGGAAAGTGGTTTTCAGATGAAGGCAATCAAGGTGACAG 2073
Db
1246 GACAATAACCCCTTTGTGATTTTCAAGGAAAGTGGTTTTCAGATGAAGGCAATCAAGGTGACAG 1305
QY
2074 CTCTGGAAGAACCAAAATTTGCTGATTTCAAAGGGAATACCTTTAGTCTTTCAGATTTCT 2133
Db
1306 CTCTGGAAGAACCAAAATTTGCTGATTTCAAAGGGAATACCTTTAGTCTTTCAGATTTCT 1365
QY
2134 GTCTCTGATATCCCCATTTCTCTGGAGAAATTAACCAATTCATCTGCTGCCAGGAGTC 2193
Db
1366 GTCTCTGATATTTCCCTTCTCTGGAGAAATTAACCAATTCATCTGCTGCCAGGAGTC 1425
QY
2194 CCGTTCTCCCGCGTGTGGTGAAGTAAACCGGAGCCCTGCACTGTGCTTCTCCCTGGAG 2253
Db
1426 CCGTTCTCCCGCGTGTGGTGAAGTAAACCGGAGCCCTGCACTGTGCTTCTCCCTGGAG 1485
QY
2254 CGTTATACGCCCACTACCAACCCAGTGTCTGCAAAATCTGCAATTCGGCAGCTCAAGGC 2313
Db
1486 CGTTATACGCCCACTACCAACCCAGTGTCTGCAAAATCTGCAATTCGGCAGCTCAAGGC 1545
QY
2314 CATGACAGATCTCTCAAGTGCAGACATCAATCTTAGAGATGTAACGAGAAACCATCACT 2373
```

```
Db
1546 CATGAACAGATCTCTCAAGTGCAGACATCAATCCTAGAGAGTGAAACGAGAAACCATCACT 1605
QY
2374 TTCTTCGCAACAGAGAGACAGACTTTTCCCTGCAAGACTGGCCCAAGGCTTTCAAAATT 2433
Db
1606 TTCTTCGCAACAGAGAGACAGACTTTTCCCTGCAAGACTGGCCCAAGGCTTTCAAAATT 1665
QY
2434 CCTTACTCCATCAGACAGCGGATTTGTGTACATTTGATACCCCAATGCCAAGGCAAG 2493
Db
1666 CCTTACTCCATCAGACAGCGGATTTGTGTACATTTGATACCCCAATGCCAAGGCAAG 1725
QY
2494 GACTGCGAGATGTTAGCACAGAAAAACAGCATCAACAGGAAATTTATCTTATTTTCGTACA 2553
Db
1726 GACTGCGAGATGTTAGCACAGAAAAACAGCATCAACAGGAAATTTATCTTATTTTCGTACA 1785
QY
2554 CAAAGTAGCCCATCTGCTGTCTTGTGAAACCTGTGGAAAGCTGTCATCAGCATGATGGT 2613
Db
1786 CAAAGTAGCCCATCTGCTGTCTTGTGAAACCTGTGGAAAGCTGTCATCAGCATGATGGT 1845
QY
2614 GATCTTTGACTCCCTGCGCTGTGCTTGAAGAGATTTGGAGAGACACACAGAAACTCTCA 2673
Db
1846 GATCTTTGACTCCCTGCGCTGTGCTTGAAGAGATTTGGAGAGACACACAGAAACTCTCA 1905
QY
2674 AACATTTCAAAATCCAGACTTGTATGAAGCCGACTTCAACTACAGCAGCAAAATGGACTC 2733
Db
1906 AACATTTCAAAATCCAGACTTGTATGAAGCCGACTTCAACTACAGCAGCAAAATGGACTC 2733
QY
2734 TAG 2736
Db
1966 TAG 1968
```

## RESULT 15

```
US-10-798-721-1
; Sequence 1, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/10/798,721
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-721-1
```

```
Query Match 59.9%; Score 1640; DB 18; Length 1734;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ATGGGAGAGCGCGGCGCACCGCAGCGCGCGGCGGAGGGCGCGCTGGCTCCCGTGG 60
Db 1 ATGGGAGAGCGCGGCGCACCGCAGCGCGCGGCGGAGGGCGCGCTGGCTCCCGTGG 60
QY 61 CTGGGGCTGTGCTTCTGGCGGAGGACCGCGGCTGCCCGAGAACTGA CAATGGCGAA 120
Db 61 CTGGGGCTGTGCTTCTGGCGGAGGACCGCGGCTGCCCGAGAACTGA CAATGGCGAA 120
QY 121 GCCCTTCCCGAATCCCATCCCATCAGCTCTCGGACACTGCTCATTTATAGAGAGCCA 180
Db 121 GCCCTTCCCGAATCCCATCCCATCAGCTCTCGGACACTGCTCATTTATAGAGAGCCA 180
QY 181 GATGATGCTTATATTATCAAGAGCAACCCCTATTGCACTCAGGTGCAAGGCGAGCCAGCC 240
Db 181 GATGATGCTTATATTATCAAGAGCAACCCCTATTGCACTCAGGTGCAAGGCGAGCCAGCC 240
```

QY 241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCAGCTCTGTGAA 300  
 Db |||||  
 241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCAGCTCTGTGAA 300  
 QY 301 GAGACTCTGACGAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTACTAGG 360  
 Db |||||  
 301 GAGACTCTGACGAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTACTAGG 360  
 QY 361 CAACAGGTGAGGAGCTTCCATGGCCCGGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420  
 Db |||||  
 361 CAACAGGTGAGGAGCTTCCATGGCCCGGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420  
 QY 421 CACCTGGGTACCTCCAAAGAGCAGGAAGCCCTCTGTGGCGATAGCCTATTTCACGGAATAAC 480  
 Db |||||  
 421 CACCTGGGTACCTCCAAAGAGCAGGAAGCCCTCTGTGGCGATAGCCTATTTCACGGAATAAC 480  
 QY 481 TTTGAAACAAGACCCCAAGGAAGGAAAGTTCCCATTTGAAGGCATGATGTACTGCACTGC 540  
 Db |||||  
 481 TTTGAAACAAGACCCCAAGGAAGGAAAGTTCCCATTTGAAGGCATGATGTACTGCACTGC 540  
 QY 541 CGCCACACAGAGGAGTCCCTGCTGCGAGGTGGATGGCTGAAATGAAGAGCCCATTT 600  
 Db |||||  
 541 CGCCACACAGAGGAGTCCCTGCTGCGAGGTGGATGGCTGAAATGAAGAGCCCATTT 600  
 QY 601 GACTCTGAACAAGACGAGAAATTTGACACAGGGCTGACCATTAACCTGTATCATCAGGCAG 660  
 Db |||||  
 601 GACTCTGAACAAGACGAGAAATTTGACACAGGGCTGACCATTAACCTGTATCATCAGGCAG 660  
 QY 661 GCACGGGTCTCGGACTCAGGAAATTTACACCTGATGGCAGCCAACTCGTGGCTAAGAGG 720  
 Db |||||  
 661 GCACGGGTCTCGGACTCAGGAAATTTACACCTGATGGCAGCCAACTCGTGGCTAAGAGG 720  
 QY 721 AGAAGCCTGTGCGCCACTGTGTGGTCTACGTGATGGGAGTGGGAAGTGTGGAGCGAA 780  
 Db |||||  
 721 AGAAGCCTGTGCGCCACTGTGTGGTCTACGTGATGGGAGTGGGAAGTGTGGAGCGAA 780  
 QY 781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGCACCAACC 840  
 Db |||||  
 781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGCACCAACC 840  
 QY 841 CCAGAAATGGGGGCAATTTCTGAAAGTCTAAGCCAGGAATCTGAATACTGCACAGAT 900  
 Db |||||  
 841 CCAGAAATGGGGGCAATTTCTGAAAGTCTAAGCCAGGAATCTGAATACTGCACAGAT 900  
 QY 901 GGTCTTTGCAATCTAGATAAAACCTCTTCATGAATAAAACCCCAAGCATTTGAGAAT 960  
 Db |||||  
 901 GGTCTTTGCAATCTAGATAAAACCTCTTCATGAATAAAACCCCAAGCATTTGAGAAT 960  
 QY 961 GCCAGCGACATTCCTTTGTACTCGGGCTTGGGTGCTGCGGTGCTGGCGGTGCGAGTCCCTG 1020  
 Db |||||  
 961 GCCAGCGACATTCCTTTGTACTCGGGCTTGGGTGCTGCGGTGCTGGCGGTGCGAGTCCCTG 1020  
 QY 1021 GTCAATTTGGTGTACCCCTTTACAGACGGAGCCAGATGACTATGGCGTGGACGTCATTGAC 1080  
 Db |||||  
 1021 GTCAATTTGGTGTACCCCTTTACAGACGGAGCCAGATGACTATGGCGTGGACGTCATTGAC 1080  
 QY 1081 TCTTCTGCAATTTGACAGTGGCTTCCAGACTTCAACCTTCAAAACAGTCCGTCAAGCCAAG 1140  
 Db |||||  
 1081 TCTTCTGCAATTTGACAGTGGCTTCCAGACTTCAACCTTCAAAACAGTCCGTCAAGCCAAG 1140  
 QY 1141 AATATCATGGAATTAATGATAAAGAAAAATCCTTTGGTAACCTCCCTGCTCTGGAATTTCT 1200  
 Db |||||  
 1141 AATATCATGGAATTAATGATAAAGAAAAATCCTTTGGTAACCTCCCTGCTCTGGAATTTCT 1200  
 QY 1201 GCCATGAGCCAGATCTGACAGTGGCCGAGCATACAGGGAGCCCATCTGTCTGCAGGAC 1260  
 Db |||||  
 1201 GCCATGAGCCAGATCTGACAGTGGCCGAGCATACAGGGAGCCCATCTGTCTGCAGGAC 1260  
 QY 1261 CCTCTGGACAAGGAGCTCATGACAGAGTCTCTACTCTTTAAACCTTTTGGGACATCAAA 1320  
 Db |||||  
 1261 CCTCTGGACAAGGAGCTCATGACAGAGTCTCTACTCTTTAAACCTTTTGGGACATCAAA 1320

QY 1321 GTCAAAAGTCCAGAGCTCGTTTCATGGTTTCCCTGGAGTGTCTGAGAGAGCTGAGTACCAC 1380  
 Db |||||  
 1321 GTCAAAAGTCCAGAGCTCGTTTCATGGTTTCCCTGGAGTGTCTGAGAGAGCTGAGTACCAC 1380  
 QY 1381 GGCAGAATCATTTCCAGGACTTTTCCCATGGAAAAACAACAGCTTTAGTACAATGCAAT 1440  
 Db |||||  
 1381 GGCAGAATCATTTCCAGGACTTTTCCCATGGAAAAACAACAGCTTTAGTACAATGCAAT 1440  
 QY 1441 CCCAGAAATAAATATGCCCTACATCCAAATCTGTCTCATCTCCCAACAGGACAGAACTG 1500  
 Db |||||  
 1441 CCCAGAAATAAATATGCCCTACATCCAAATCTGTCTCATCTCCCAACAGGACAGAACTG 1500  
 QY 1501 AGGACAACTGCTGCTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTG 1560  
 Db |||||  
 1501 AGGACAACTGCTGCTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTG 1560  
 QY 1561 AGCTTACTCATACCAACAGCGTGCATCCAGAGGAGAAATTTCTTTGGAGATTTTATATGTC 1620  
 Db |||||  
 1561 AGCTTACTCATACCAACAGCGTGCATCCAGAGGAGAAATTTCTTTGGAGATTTTATATGTC 1620  
 QY 1621 ATCAACCAAGGTGAACCCAG 1640  
 Db |||||  
 1621 ATCAACCAAGGTGAACCCAG 1640

Search completed: April 1, 2005, 06:11:22  
 Job time : 1527 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: March 31, 2005, 20:54:14 ; Search time 11586 Seconds  
(without alignments)  
11442.557 Million cell updates/sec

Title: US-10-798-721-9  
Perfect score: 2736  
Sequence: 1 atggggagagcggcgccac.....gcaggcaaatggactcttag 2736

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hcg.\*
- 3: gb\_in.\*
- 4: gb\_cm.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sv.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2462.4	90.0	3252	9 AY358147	Homo sapi
2	2365.2	86.4	7002	6 BD162193	Novel unc
3	2365.2	86.4	7002	9 AB055056	Homo sapi
4	2284	83.5	2868	6 AX800719	Sequence
5	2220	81.1	2661	6 AX800717	Sequence
6	1982.6	72.5	3925	10 MMU487854	Mus muscu
7	1599.8	58.5	2448	6 CQ841583	Sequence
8	1599.8	58.5	2448	9 AK122610	Homo sapi
9	641.6	23.5	2625	6 CQ721377	Sequence
10	638.4	23.3	2585	6 CQ842137	Sequence
11	638.4	23.3	2585	9 AK122615	Homo sapi
12	597	21.8	2860	6 AX686445	Sequence
13	592.2	21.6	2860	6 AX686447	Sequence
14	590.2	21.6	3933	6 CQ850929	Sequence
15	590.2	21.6	3933	9 AK128132	Homo sapi
16	590.2	21.6	3935	9 AB096256	Homo sapi
17	589	21.5	3770	9 AY126437	Homo sapi
18	588.6	21.5	3884	6 AR528525	Sequence
19	588.6	21.5	3884	6 AX464012	Sequence

20	588.6	21.5	3884	9 AY358351	Homo sapi
21	572.4	20.9	2895	6 AX512281	Sequence
22	569	20.8	3788	10 MMU487853	Mus muscu
23	564.8	20.6	3672	10 BC048162	Mus muscu
24	564.8	20.6	3672	10 BC057560	Mus muscu
25	563.2	20.6	2838	10 RN087306	Mus muscu
26	554	20.2	2832	5 AY099459	Xenopus laevis
27	544	19.9	2831	6 BD057526	Netrin re
28	537	19.6	2995	6 AX497288	Sequence
29	527.4	19.3	9328	10 AB118026	Rattus no
30	520.6	19.0	2962	5 AY187310	Gallus ga
31	519.2	19.0	3646	6 CQ881060	Sequence
32	519.2	19.0	3646	9 AF055634	Homo sapi
33	518.4	18.9	9299	10 MMU72634	Mus muscu
34	493.4	18.0	3992	10 MMU487852	Mus muscu
35	491.8	18.0	2697	6 AX451652	Sequence
36	487	17.8	2697	6 AX268596	Sequence
37	487	17.8	2697	10 RN087305	Rattus nor
38	487	17.8	2752	6 AX449572	Sequence
39	487	17.8	3014	6 BD057524	Netrin re
40	474.4	17.3	2986	6 CQ881052	Sequence
41	467.2	17.1	2881	6 AX527916	Sequence
42	458.2	16.7	1223	6 CQ720317	Sequence
43	457.4	16.7	3844	10 BC058084	Mus muscu
44	442.2	16.2	3580	6 AX367094	Sequence
45	399.8	14.6	2406	6 AX833115	Sequence

## ALIGNMENTS

RESULT 1	AY358147	3252 bp	mRNA	linear	PRI 03-OCT-2003
LOCUS	Homo sapiens clone DNA219246 UNQ6012	UNQ6012	complete cds.		
DEFINITION	AY358147				
ACCESSION	AY358147.1	GI:37181401			
VERSION	FLI_CDNA				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 3252)				
AUTHORS	Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Wandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.				
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment				
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)				
PUBLISHED	12975309				
REFERENCE	2 (bases 1 to 3252)				
AUTHORS	Clark, H.F.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA				
FEATURES	Location/Qualifiers				
source	1..3252				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="DNA219246"				
gene	1..3252				
	/locus_tag="UNQ6012"				
CDS	329..3190				
	/locus_tag="UNQ6012"				
	/notes="PRO34692"				

```

/codon_start=1
/product="UNC5D"
/protein_id="AA088514.1"
/db_xref="GI:37181402"
/translation="MGRAAATAGGGGARRWLPWLGCTFWAAGTAARCTDNGEALPE
SIPAPGTLPHFIEEDDAYIITKSNPIALRCARPAQOIFKNGEWVHONHVEET
LDESSGLKREYFINTVROQVEDFHGPDYWCQVAMSHLGTSKRKASRYAIRLKN
FEODPQGRVEYEGMVLVLRPEGVPAAEVLKNEEPIIDSEQDENIDRADHNLII
ROARLSDGNTCTMAANIIVAKRRSLSATVVVYVNGWSSWTEWSACNVCGRGWOKRS
RCTNPAIPLNGAFCEGMSVKITCTSLCPVDGSEVMSVCSPECHELIRCTA
PPRNGGKCEGLSQSENCTDGLCILDKKPLHEIKPQSIENASDIALYSLGAAVVA
VAVLVIGTVLRRSDYGVDDIDSSALTGFTQFNKTVROGNSLLLSNAMPDITV
SNTYSGPILCLQDLDELMTESLNFPLSDIKVQSSFMVSLGVSERAEYRGKHSR
TFPHGNHSHFYMSPRNKMPYIQNLSSLPRTTELRTGVFHLGRLVMPNTGVSLLI
PHGAIPEENSWEIYMINOPELSQSDSEVLSPVTCGPPDMIWTFPTALTIPHCA
DYSSEHWHLKRYTQCKWESVMSVEDSTCYCLLDPPACHVLLDSFGTYALRCEP
IDYCAVKQLXVAFVGCMSNLDYLNRYICVDNTPCAFOEVVSDERHQGGQLLEPKL
LHPKGNFSLQISVLDDIPPLMLRIKPTACQEPFSPVSNRQPLHCAFSLERYPT
TTQLSKICIROLKHEQILOVQTSILESERTITPFAQEDSTFPQAQTPKAFKIPYS
IRQICATPDTNPKGDKWMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQHDGD
LDSLALAEIEIGRTHTKLSNISQSOLDDEADFNYSRQNGE"

```

ORIGIN

Query Match 90.0%; Score 2462.4; DB 9; Length 3252;

Best Local Similarity 92.7%; Pred. No. 0;

Matches 2693; Conservative 0; Mismatches 1; Indels 210; Gaps 2;

QY	1	ATGGGAGAGCGCGCCACCGCAGCGCGGCGGAGGGCGCGCGCTGGCTCCCGTGG	60
DB	329	ATGGGAGAGCGCGCGCCACCGCAGCGCGGCGGAGGGCGCGCGCTGGCTCCCGTGG	388
QY	61	CTGGGGCTGTGCTTCTGGGCGGAGGACCGCGGCTGCCGAGGAACTGACAAATGCGGAA	120
DB	389	CTGGGGCTGTGCTTCTGGGCGGAGGACCGCGGCTGCCGAGGAACTGACAAATGCGGAA	448
QY	121	GCCTTCCGGAATCCATCCCATCAGCTCTCTGGGACACTGCTCATATTTATAGAGAGCCA	180
DB	449	GCCTTCCGGAATCCATCCCATCAGCTCTCTGGGACACTGCTCATATTTATAGAGAGCCA	508
QY	181	GATGATGCTTATATATCAAGAGCAACCTATTGCACTCAGGTGCAAGCGGCGCAGCC	240
DB	509	GATGATGCTTATATATCAAGAGCAACCTATTGCACTCAGGTGCAAGCGGCGCAGCC	568
QY	241	ATGCAGATATCTTCAAAATGCAACGGCGAGTGGTCCATCAGAACGAGCAGCTCTCTGAA	300
DB	569	ATGCAGATATCTTCAAAATGCAACGGCGAGTGGTCCATCAGAACGAGCAGCTCTCTGAA	628
QY	301	GAGACTCTGACGAGAGCTCAGGTTTGAAGGTCGCGGAAAGTGTTCATCAATGTTACTAGG	360
DB	629	GAGACTCTGACGAGAGCTCAGGTTTGAAGGTCGCGGAAAGTGTTCATCAATGTTACTAGG	688
QY	361	CAACAGGTGAGGACTTCCATGCGCCGAGGACTATTGTCAGGTCAGGTGGCGTGGAGC	420
DB	689	CAACAGGTGAGGACTTCCATGCGCCGAGGACTATTGTCAGGTCAGGTGGCGTGGAGC	748
QY	421	CACCTGGGTACCTCCAAAGAGCAGGAAGGCTCTGTGCGCATAGCCTATTATACGGAAAAAC	480
DB	749	CACCTGGGTACCTCCAAAGAGCAGGAAGGCTCTGTGCGCATAGCCTATTATACGGAAAAAC	808
QY	481	TTTGAAACAAGACCAACAAGGAAGGAAGTTCCCATTTGAAGGCAATGTTGTACTGCACTGC	540
DB	809	TTTGAAACAAGACCAACAAGGAAGGAAGTTCCCATTTGAAGGCAATGTTGTACTGCACTGC	868
QY	541	CGCCCCACGAGGGAGTCCCTGTCGCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATTT	600
DB	869	CGCCCCACGAGGGAGTCCCTGTCGCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATTT	928
QY	601	GACTCTGAACAAGACGAGAACTTGAACACAGGGCTGACCAATACCTGATCATCAGGCAG	660
DB	929	GACTCTGAACAAGACGAGAACTTGAACACAGGGCTGACCAATACCTGATCATCAGGCAG	988
QY	661	GCAGGCTCTGAGACTCAGGAATATACCTGATGCGCAGCCAACTCTGGCTAGAGG	720

DB	989	GCACGGCTCTCGGACTCAGGAAATTAACCTGCATGGCAGCAACATCGTGCTAAGAGG	1048
QY	721	AGAAGCTGTGCGGCCACTGTTGTGTGTCTAC	750
DB	1049	AGAAGCTGTGCGGCCACTGTTGTGTGTCTACGTAATGAGGGTGTCTTCTCTGGACAGAG	1108
QY	751	-----	750
DB	1109	TGGTCAGCTGCAATGTTGCTGTGTGTAGAGGATGGCAGAAACGTTTCCGGACCTGCACC	1168
QY	751	-----	750
DB	1169	AACCCAGCTCTCTCAATGTTGGGGCTTTTGTGAGGGAATGTCAGTGCGAGAAAAATAACC	1228
QY	751	-----GTGATGGGAGCTGGGAAGTGTGAGCGAAATGGTCCGCTCTGC	792
DB	1229	TGCACCTTCTTGTCTGTGGATGGGAGTGGGAAGTGTGAGCGAATGGTCCGCTCTGC	1288
QY	793	AGTCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCAACCCCGGAGAAATGGG	852
DB	1289	AGTCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCAACCCCGGAGAAATGGG	1348
QY	853	GGCAATTTCTGGAAGTCTAAGCCAGGAACTCTGAAAATCTGCACAGATGGTCTTTGCATC	912
DB	1349	GGCAATTTCTGGAAGTCTAAGCCAGGAACTCTGAAAATCTGCACAGATGGTCTTTGCATC	1408
QY	913	CTAGATAAAAAACCTCTTTCATGAAATAAAACCCCAAGCATTTGAGAAATGCCAGCGACATT	972
DB	1409	CTAGATAAAAAACCTCTTTCATGAAATAAAACCCCAAGCATTTGAGAAATGCCAGCGACATT	1468
QY	973	GCTTTGTACTCGGGCTTGGGTCTCGCTGCTGGCGCTTGGCGCTTGGTCTCTTGGTCTC	1032
DB	1469	GCTTTGTACTCGGGCTTGGGTCTCGCTGCTGGCGCTTGGCGCTTGGTCTCTTGGTCTC	1528
QY	1033	ACCTTTTACAGCGAGCGACGAGTGCATATGCGGTGCGTGCATTTGACTCTTCTGCTGATG	1092
DB	1529	ACCTTTTACAGCGAGCGAGTGCATATGCGGTGCGTGCATTTGACTCTTCTGCTGATG	1588
QY	1093	ACAGTGGCTTCCAGACCTTCAATTTCAAAAACAGTCCGTCAGCAAGCAAGAAATATCATGGAA	1152
DB	1589	ACAGTGGCTTCCAGACCTTCAATTTCAAAAACAGTCCGTCAGCAAGCAAGAAATATCATGGAA	1630
QY	1153	CTAATGATACAAGAAAAATCTCTTGGTAACTCCCTGCTCTCTGAAATCTGCAATTCGCAATGCGCA	1212
DB	1631	-----GGTAACTCCCTGCTCTCTGAAATCTGCAATTCGCAATTCGCAATGCGCA	1666
QY	1213	GATCTGAGTGCAGCGGACATACAGCGGACCCATCTGTCAGGACCCCTCTGAGCAAG	1272
DB	1667	GATCTGAGTGCAGCGGACATACAGCGGACCCATCTGTCAGGACCCCTCTGAGCAAG	1726
QY	1273	GAGCTCATGACAGAGTCTCTCACTTTTAAACCTTTGTGCGACATCAAAAGTGAAGTCCAG	1332
DB	1727	GAGCTCATGACAGAGTCTCTCACTTTTAAACCTTTGTGCGACATCAAAAGTGAAGTCCAG	1786
QY	1333	AGCTCGTTCAATGGTTTCCCTGGGAGTGTCTGAGAGAGTGAATACACGGGAGAAATCAT	1392
DB	1787	AGCTCGTTCAATGGTTTCCCTGGGAGTGTCTGAGAGAGTGAATACACGGGAGAAATCAT	1846
QY	1393	TCCAGGACTTTTCCCATGGAACCAACACGCTTTAGTACAAATGCATCCCAAGAAATAAA	1452
DB	1847	TCCAGGACTTTTCCCATGGAACCAACACGCTTTAGTACAAATGCATCCCAAGAAATAAA	1906
QY	1453	ATGCCCTACATCAAAAATCTGTCACTCTCCCAAGGACAGAACTGAGGACAACTGGT	1512
DB	1907	ATGCCCTACATCAAAAATCTGTCACTCTCCCAAGGACAGAACTGAGGACAACTGGT	1966
QY	1513	GTCTTTGGCCATTAGGGGGGCTTATGTAATGCCAAATACAGGGGTGAGCTTACTCATA	1572
DB	1967	GTCTTTGGCCATTAGGGGGGCTTATGTAATGCCAAATACAGGGGTGAGCTTACTCATA	2026
QY	1573	CCACAGGTGCCATCCAGAGGAGAAATTTCTGGGAGATTTATATGTCCATCAACCAAGGT	1632
DB	2027	CCACAGGTGCCATCCAGAGGAGAAATTTCTGGGAGATTTATATGTCCATCAACCAAGGT	2086

Qy	1633	GAACCCAGCCTC	CAGTCAGATGGGCTCTGAGGTGCTCTCTGAGTCTCTGAAGTCACTGTGGT	1692
Db	2087	GAACCCAGCCTC	CAGTCAGATGGGCTCTGAGGTGCTCTCTGAGTCTCTGAAGTCACTGTGGT	2146
		CCTCCAGACATGATCGTCACCACTCCCTTTTGCAATTGACCACTCCCGCACTGTGCAGATGTC	1752	
Db	2147	CCTCCAGACATGA	TCGTCAACACTCCCTTTGCAATTGACCACTCCCGCACTGTGCAGATGTC	2206
Qy	1753	AGTTCTGAGCAT	ATGGAAATATCCATTTAAAGAAGAGGACACAGCAGGCGCAAAATGGAGGAA	1812
Db	2207	AGTTCTGAGCAT	ATGGAAATATCCATTTAAAGAAGAGGACACAGCAGGCGCAAAATGGAGGAA	2266
Qy	1813	GTGATGTCAGT	GAAGATGAATCTACATCCGTGTTACTGCGCTTTTGGACCCCTTTGGACCCCTTTGGCCGTG	1872
Db	2267	GTGATGTCAGT	GAAGATGAATCTACATCCGTGTTACTGCGCTTTTGGACCCCTTTGGACCCCTTTGGCCGTG	2326
Qy	1873	CATGTGCTCCT	GGACAGCTTTGGGACCTATGCGCTCACTGCGAGGCCAAATCACAGACTGT	1932
Db	2327	CATGTGCTCCT	GGACAGCTTTGGGACCTATGCGCTCACTGCGAGGCCAAATCACAGACTGT	2386
Qy	1933	GCCGTGAAGCAA	CTGAAAGTGCGGTTTTTGGCTGCAATGCTCTGTAACTCCCTGGATTAC	1992
Db	2387	GCCGTGAAGCAA	CTGAAAGTGCGGTTTTTGGCTGCAATGCTCTGTAACTCCCTGGATTAC	2446
Qy	1993	AACTTTGAGAGTT	ACTGTTGGACAAATACCCCTTGTGCATTTACAGGAAGTGGTTTCAGAT	2052
Db	2447	AACTTTGAGAGTT	ACTGTTGGACAAATACCCCTTGTGCATTTACAGGAAGTGGTTTCAGAT	2506
Qy	2053	GAAGAGGCAT	CAAGGTGGACAGCTCCTCGAAGAACCAAAATTCGTGCAATTTCAAAGGGAAT	2112
Db	2507	GAAGAGGCAT	CAAGGTGGACAGCTCCTCGAAGAACCAAAATTCGTGCAATTTCAAAGGGAAT	2566
Qy	2113	ACCTTTAGTCT	TTTCAGATTTCTGAGATTTCTGTCCTTGATATCCCCCATTCCTCTCGAGAAATPAAACCA	2172
Db	2567	ACCTTTAGTCT	TTTCAGATTTCTGAGATTTCTGTCCTTGATATCCCCCATTCCTCTCGAGAAATPAAACCA	2626
Qy	2173	TTCACTGCGTC	GCGAGGAGTCCGCTTCTCCGCGGTGTTGGTGCAGTACCCGCGACCCCTG	2232
Db	2627	TTCACTGCGTC	GCGAGGAGTCCGCTTCTCCGCGGTGTTGGTGCAGTACCCGCGACCCCTG	2686
Qy	2233	CACGTGCTCT	TCTCCCTGGAGCGTTATACGCCCACTACCAACCAGCTGTCTCTGCAAAATC	2292
Db	2687	CACGTGCTCT	TCTCCCTGGAGCGTTATACGCCCACTACCAACCAGCTGTCTCTGCAAAATC	2746
Qy	2293	TGCATTCGGC	AGCTCAAAGGCATGAACAGATCTCCAAAGTGCGAGACATCAATCTCTAGAG	2352
Db	2747	TGCATTCGGC	AGCTCAAAGGCATGAACAGATCTCCAAAGTGCGAGACATCAATCTCTAGAG	2806
Qy	2353	AGTCAACGAGAA	ACCATCATTCTTCGCACAAGGAGCAGCACTTTCCCTGCGACAGACT	2412
Db	2807	AGTCAACGAGAA	ACCATCATTCTTCGCACAAGGAGCAGCACTTTCCCTGCGACAGACT	2866
Qy	2413	GGCCCCAAAG	CTTCAAATTTCCCTACTCTCATCAGACAGCGGATTTGTGCTACATTTGAT	2472
Db	2867	GGCCCCAAAG	CTTCAAATTTCCCTACTCTCATCAGACAGCGGATTTGTGCTACATTTGAT	2926
Qy	2473	ACCCCCAATG	CAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGG	2532
Db	2927	ACCCCCAATG	CAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGG	2986
Qy	2533	AATTTATCTT	ATTTTGGCTACCAAGATAGCCCATCTGCTGTCAATTTTGAACCTGTGGAA	2592
Db	2987	AATTTATCTT	ATTTTGGCTACCAAGATAGCCCATCTGCTGTCAATTTTGAACCTGTGGAA	3046
Qy	2593	GCTCGTCAT	CAGCATGATGGTGAATCTTGACTCCCTGGCTGTGCGCTTGAAGAGATTGGG	2652
Db	3047	GCTCGTCAT	CAGCATGATGGTGAATCTTGACTCCCTGGCTGTGCGCTTGAAGAGATTGGG	3106
Qy	2653	AGGACACAC	GAAATCTCTCAAAATTTTCAGAAATCCAGCTTGATGAAGCGGACTTCAAC	2712
Db	3107	AGGACACAC	GAAATCTCTCAAAATTTTCAGAAATCCAGCTTGATGAAGCGGACTTCAAC	3166

QY	2713	TACAGCAGGCAAAATGGACTCTAG	2736
Db	3167	TACAGCAGCAAAATGGACTCTAG	3190
RESULT 2			
BD162193			
LOCUS	BD162193	7002 bp	DNA linear PAT 17-JAN-2003
DEFINITION	Novel unc5H4 gene and protein encoded thereby.		
ACCESSION	BD162193		
VERSION	BD162193.1	GI:27867951	
KEYWORDS	JP 2002153290-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 7002)		
JOURNAL	Ohara,O., Nagase,T., Nakayama,M. and Nakajima,D.		
COMMENT	Novel unc5H4 gene and protein encoded thereby Patent: JP 2002153290-A 1 28-MAY-2002; KAZUSA DNA RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002153290-A/1 PD 28-MAY-2002 PF 19-DEC-2000 JP 2000385090 PI OSMU OHARA, TAKAHIRO NAGASE, MANABU NAKAYAMA, DAISUKE NAKAJIMA PC C12N15/09,C07K14/705,C12N15/00 CC Novel unc5H4 gene and protein encoded thereby FH Key Location/Qualifiers FT CDS (56)..(2899).		
FEATURES	Location/Qualifiers		
source	1..7002		
ORIGIN	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
Query Match	86.4%; Score 2365.2; DB 6; Length 7002;		
Best Local Similarity	92.4%; Pred. No. 0;		
Matches 2597; Conservative 0; Mismatches 3; Indels 210; Gaps 2;			
QY	95	CTGCCCGAGGAACTCACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGA	154
Db	135	CTTCACCAGGAACCTGACAAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGA	194
QY	155	CAC TGCCCTCATTTTCATAGAGAGCCAGATGCTTATTATTAACAAGACACCCTATTG	214
Db	195	CAC TGCCCTCATTTTCATAGAGAGCCAGATGCTTATTATTAACAAGACACCCTATTG	254
QY	215	CAC TCAGGTGC AAGACGAGGCCAGCCATGCAGATATTTCTCAAATGC AA CGGCAGTG GG	274
Db	255	CAC TCAGGTGC AAGACGAGGCCAGCCATGCAGATATTTCTCAAATGC AA CGGCAGTG GG	314
QY	275	TCCATCAGAACGAGCACGCTCTCTGAAGAGACTCTGGACGAGCTCAGGTTTTGAAGTGCC	334
Db	315	TCCATCAGAACGAGCACGCTCTCTGAAGAGACTCTGGACGAGCTCAGGTTTTGAAGTGCC	374
QY	335	GCGAAGTGTTCATCAATGTTACTTAGGC AAC AGGTGGAGGACTTCCTCATGGGCCCGAGGACT	394
Db	375	GCGAAGTGTTCATCAATGTTACTTAGGC AAC AGGTGGAGGACTTCCTCATGGGCCCGAGGACT	434
QY	395	ATTGGTGCCAGTGTGGCGTGGAGGCCACCTGGGTACTCTCAACAGCAGGAAGGCCCTCTG	454
Db	435	ATTGGTGCCAGTGTGGCGTGGAGGCCACCTGGGTACTCTCAACAGCAGGAAGGCCCTCTG	494
QY	455	TGCGCATAGCCCTATTTCACGAAAAAATTTTGAAACAAGAACCCCAACAAGGAAGGGAAGTCCCCA	514
Db	495	TGCGCATAGCCCTATTTCACGAAAAAATTTTGAAACAAGAACCCCAACAAGGAAGGGAAGTCCCCA	554
QY	515	TTGAAGGCAATGATTGTACTGCATGCGGCCCAACAGAGGGAGTCCCTGCTGCCAGGTGG	574
Db	555	TTGAAGGCAATGATTGTACTGCATGCGGCCCAACAGAGGGAGTCCCTGCTGCCAGGTGG	614

QY	575	AATGGCTGAAAATGAAGAGCCCAATTGACTCTTGAAACAAGACAGAGAAACATTGACACACAGGG	634	DB	1653	CAAGGACAGAACTGAGGACAACCTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGC	1712
DB	615	AATGGCTGAAAATGAAGAGCCCAATTGACTCTTGAAACAAGACAGAGAAACATTGACACACAGGG	674	QY	1547	CAAATACAGGGGTGAGCTTACTCATAACAACGGTGCATCCAGAGAGAGAAATCTTTGGG	1606
QY	635	CTGACCATAACTGATCATCAGGCAAGGACCGGCTCTCGGACTCAGGAAATTAACCTGCA	694	DB	1713	CAAATACAGGGGTGAGCTTACTCATAACAACGGTGCATCCAGAGAGAGAAATCTTTGGG	1772
DB	675	CTGACCATAACTGATCATCAGGCAAGGACCGGCTCTCGGACTCAGGAAATTAACCTGCA	734	QY	1607	AGATTATATGTCCATCAACAAAGGTGAACCCAGCTCCAGTCAAGTGGCTCTCAGGGTGC	1666
QY	695	TGGCAGCAACATCGTGGCTTAAGAGGAGAGAGCGCTCTCGGCCACATGTTGTGTCTAC	750	DB	1773	AGATTATATGTCCATCAACAAAGGTGAACCCAGCTCCAGTCAAGTGGCTCTCAGGGTGC	1832
DB	735	TGGCAGCAACATCGTGGCTTAAGAGGAGAGAGCGCTCTCGGCCACATGTTGTGTCTAC	794	QY	1667	TCCTGAGTCTGAGAGTCACTGTGGTCCCTCAGACATGATCGTCAACCTCCCTTTGCA	1726
QY	751	-----	750	DB	1833	TCCTGAGTCTGAGAGTCACTGTGGTCCCTCAGACATGATGATCGTCAACCTCCCTTTGCA	1892
DB	795	ATGGAGGCTGGTCTTCTCTGACAGAGTGTGACGCTGCAATGTTTCGCTGTGTAGAGAT	854	QY	1727	TGACCATCCCGCACTGTGCAGATGTCACTTCTGAGCATTTGGAATATCCATTTAAAGAGA	1786
QY	751	-----	750	DB	1893	TGACCATCCCGCACTGTGCAGATGTCACTTCTGAGCATTTGGAATATCCATTTAAAGAGA	1952
DB	855	GGCAGAAACGTTCCCGGACCTGCAACCAACAGCTCCTCTCAATGGTGGGCGCTTTTGTG	914	QY	1787	GGACACAGCAGGGCAAAATGGGAGGAAATGATGTCACTGAGTGAAGATCAATCTACATCCTGTT	1846
QY	751	-----	766	DB	1953	GGACACAGCAGGGCAAAATGGGAGGAAATGATGTCACTGAGTGAAGATCAATCTACATCCTGTT	2012
DB	915	AGGAAATGTCAGTGACGAAAAATAACCTGCACTTCTTCTTGTCTGTGATGGGAGCTGGG	974	QY	1847	ACTGCCTTTTGGACCCCTTTTGGTGTCTCATGTGCTCTCGACAGCTTTTGGGACCTATGCGC	1906
QY	767	AAGTGTGGAGCGAATGCTCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGT	826	DB	2013	ACTGCCTTTTGGACCCCTTTTGGTGTCTCATGTGCTCTCGACAGCTTTGGGACCTATGCGC	2072
DB	975	AAGTGTGGAGCGAATGCTCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGT	1034	QY	1907	TCACCTGGAGAGCCAAATCAGACACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTGGCT	1966
QY	827	GCACAGCACACCCCGAGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAATCTG	886	DB	2073	TCACTGGAGAGCCAAATCAGACACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTGGCT	2132
DB	1035	GCAAGCACACCCCGAGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAATCTG	1094	QY	1967	GCATGTCTGTAACTCCCTCGATTAACCTTGAAGTGTACTGTGTGGACAAATACCCCTT	2026
QY	887	AAACTGCAAGATGCTTTTGCATCTAGATAAATAAACCTCTTCATGAATAAATAAACCC	946	DB	2133	GCATGTCTGTAACTCCCTCGATTAACCTTGAAGTGTACTGTGTGGACAAATACCCCTT	2192
DB	1095	AAACTGCAAGATGCTTTTGCATCTAGATAAATAAACCTCTTCATGAATAAATAAACCC	1154	QY	2027	GTGCATTTTCAGAAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCTCGGAAGAAC	2086
QY	947	AAAGCATTTGAGAAATGCCAGGACATTTGTTGATCTCGGGCTTTGGGTGCTGCGGTG	1006	DB	2193	GTGCATTTTCAGAAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCTCGGAAGAAC	2252
DB	1155	AAAGCATTTGAGAAATGCCAGGACATTTGTTGATCTCGGGCTTTGGGTGCTGCGGTG	1214	QY	2087	CAAAAATTCGCAATTTCAAAGGGGAATACCTTTTATGTCTTCAAGTTCCTTGTATATTC	2146
QY	1007	CCGTTGCAAGTCTCGGTCAATTTGGTGTCAACCTTTACAGCGGAGCCAGAGTGAATGGC	1066	DB	2253	CAAAAATTCGCAATTTCAAAGGGGAATACCTTTTATGTCTTCAAGTTCCTTGTATATTC	2312
DB	1215	CCGTTGCAAGTCTCGGTCAATTTGGTGTCAACCTTTACAGCGGAGCCAGAGTGAATGGC	1274	QY	2147	CCCAATTCCTCTGGAGAAATTAACCACTTCACTGCTGCCAGGAAGTCCCGTTCTCCCGCG	2206
QY	1067	TGGAGTCAATGACTCTTCTGCAATGACAGGTGGCTTCCAGACCTTCAACTTCAAAAACAG	1126	DB	2313	CCCAATTCCTCTGGAGAAATTAACCACTTCACTGCTGCCAGGAAGTCCCGTTCTCCCGCG	2372
DB	1275	TGGAGTCAATGACTCTTCTGCAATGACAGGTGGCTTCCAGACCTTCAACTTCAAAAACAG	1334	QY	2207	TGTGTGTGAGTAAACCGGCGAGCCCTCGCACTGTGCTTCTCCCTGGAGAGCTTATACGCCCA	2266
QY	1127	TCCGTCAAGCCAAAGAAATATCATGGAACTAATGATACAAGAAAAATCCTTTTGTATCTCC	1186	DB	2373	TGTGTGTGAGTAAACCGGCGAGCCCTCGCACTGTGCTTCTCCCTGGAGAGCTTATACGCCCA	2432
DB	1335	TCCGTCAA-----	1352	QY	2267	CTACCAACCCAGCTGCTCTGCAAAAATCTGCAATTCGGAGCTCAAAGGCCATGAACAGATCC	2326
QY	1187	TGCTCCTGAAATCTGCGAATGAGCCAGATCTGACAGTGAAGCCGAGCATACAGGAGCCCA	1246	DB	2433	CTACCAACCCAGCTGCTCTGCAAAAATCTGCAATTCGGAGCTCAAAGGCCATGAACAGATCC	2492
DB	1353	TGCTCCTGAAATCTGCGAATGAGCCAGATCTGACAGTGAAGCCGAGCATACAGGAGCCCA	1412	QY	2327	TCCAAAGTGCAGACATCAATCTTGAAGTGAACAGAGAAACCATCACTTCTTCGCAACAAG	2386
QY	1247	TCTGTCTGCGAGCCCTCTGCAAGAGAGTCTATGACAGAGTCTCACTCTTTTAAACCTT	1306	DB	2493	TCCAAAGTGCAGACATCAATCTTGAAGTGAACAGAGAAACCATCACTTCTTCGCAACAAG	2552
DB	1413	TCTGTCTGCGAGCCCTCTGCAAGAGAGTCTATGACAGAGTCTCACTCTTTTAAACCTT	1472	QY	2387	AGSACAGACTTTTCCCTGCAAGACTGCGCCCAAGGCTTCAAAAATTCCTTATCCATCA	2446
QY	1307	TGTGCGACATCAAAAGTGAAGTCCAGAGCTCGTTTCAATGTTTCCCTGGAGTGTCTGAGA	1366	DB	2553	AGSACAGACTTTTCCCTGCAAGACTGCGCCCAAGGCTTCAAAAATTCCTTATCCATCA	2612
DB	1473	TGTGCGACATCAAAAGTGAAGTCCAGAGCTCGTTTCAATGTTTCCCTGGAGTGTCTGAGA	1532	QY	2447	GACAGCGGATTTGTGCTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGT	2506
QY	1367	GAGCTGAGTACACGGCAAGATCAATTCAGGACTTTTCCCATGAGAAACCAACAGCT	1426	DB	2613	GACAGCGGATTTGTGCTACATTTGATACCCCAATGCAAGGCAAGGACTGGCAGATGT	2672
DB	1533	GAGCTGAGTACACGGCAAGATCAATTCAGGACTTTTCCCATGAGAAACCAACAGCT	1592	QY	2507	TAGCACAG	

Db 2733 CTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCC 2792

Qy 2627 TGGCCTGTGCTTGAAGAGATTGGGAGGACACACAGCAAACTCTCAAAATTCAGAAT 2686

Db 2793 TGGCCTGTGCTTGAAGAGATTGGGAGGACACACAGCAAACTCTCAAAATTCAGAAT 2852

Qy 2687 CCCAGCTTGATGAGCCGACTTCAACTACAGCAGGCAAAATGCACTTAG 2736

Db 2853 CCCAGCTTGATGAGCCGACTTCAACTACAGCAGGCAAAATGCACTTAG 2902

RESULT 3

AB055056

LOCUS AB055056 7002 bp mRNA linear PRI 08-JAN-2002

DEFINITION Homo sapiens mRNA for KIAA1777 protein (Unc5h4), complete cds.

ACCESSION AB055056

VERSION AB055056.1 GI:18150093

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Nakajima,D., Nakayama,M., Nagase,T. and Ohara,O.

TITLE Identification of unc5h4 gene

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 7002)

AUTHORS Nakajima,D., Nakayama,M., Nagase,T. and Ohara,O.

TITLE Direct Submission

JOURNAL Submitted (25-JAN-2001) Daisuke Nakajima, Kazusa DNA Research Institute, Laboratory for Genome Informatics, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:nakajima@kazusa.or.jp, Tel:81438523915, Fax:81438523914)

FEATURES

source

1..7002

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="fh19201"

/tissue\_type="brain"

/dev\_stage="adult"

/note="vector: pBluescript II SK plus"

gene

1..7002

/genes="KIAA1777"

56..2902

/genes="KIAA1777"

/note="similar to Unc5h1, Unc5h2 and Unc5h3"

/codon\_start=1

/product="KIAA1777 protein (Unc5h4)"

/protein\_id="BAB83663.1"

/db\_xref="GI:18150094"

CDS

1..2902

/translations="MILVLVKAISDVCAAGTSGFLDFSSQTPGTDNGEALPESIPSA  
PGTLPHFIEPDDAYIIKSNPIALRCKARPAMOIFPKNGEWHQNEHVSEETLDSS  
GLKRVFVFNTRFOVEDPHGVEDYQCQVAMSHLCTSKRKASVPIAVLRNEDDP  
QGREVIEGIVLHCRPPGPAAEVWLKNEEPIDESDENIDTRADNLIIRQRL  
SDSGNTCAANIAVAKRSLATVVIYVNGSWSSWESACNVRGQKRSRTCTN  
PAPLNGCATCEGNSVQKITCTSLCPVDGSEWSEWSVCSPECEHLIRIRECTAPPN  
GGFKCGLSSENCQDKILDKPLHEIKQSIENASDIALYSGLGAHVAVAVLVN  
IGTVLYRVSQSDYGVVIDSSALTGGFQTFNFKTVRQNSLLIANSAMODLTVSRTYS  
GPICLDDPKDKELMTESLLPNPLSDIKVKVQSSFVSLGVSEPAEYHGNHRTPPHG  
NHSFSTMPNRNPKPIQNLSSLPTEILRTGTGVLGRLVMPNTGVSLIIPHGAI  
PENSWEIYMSINQSPSLSQSGSEVLLSPVETCGPDMIVTTPFALTIPHCADVSSE  
HWNHLKRTQQQKWEVMSVEDESTSCYLLDPFACHVLLDSFGYALTGPITDCA  
HKLQKVAIFGCMSCNSLDNLRVYCVNDNTPCAFQVSVDERHGGQLLEPKLLHPKG  
NTPSLOISLVIDIPFLWRIKPTACQVFPFSCVNSRNPOLHCAFSLERYTPTTTL  
CKICIRLQKHEQILQVQSILSERETITFFAQEDSTFPAQTGPKPAKIPVSIORI  
CATFDPNAGKQWLAQNSINRLNLSFATQSSPSAVILNLWEARHQHGDLDLSIA  
CALEIEGRTHTKLSNISQSLDEADFNYSRQNGI"

# ORIGIN

Query Match 86.4%; Score 2365.2; DB 9; Length 7002;

Best Local Similarity 92.4%; Pred. No. 0;

Matches 2597; Conservative 0; Mismatches 3; Indels 210; Gaps 2;

Qy 95 CTGCCCGAGGAACTGA CAATGCGAAAGCCCTTCCCAGATCCATCCATCAGCTCCTCGGA 154

Db 135 CTTACACAGGAACTGA CAATGCGAAAGCCCTTCCCAGATCCATCCATCAGCTCCTCGGA 194

Qy 155 CACTGCCTCATTTTCA TAGAGGAGCCAGATGATGCTTTATATATCAAGAGCAACCTATTG 214

Db 195 CACTGCCTCATTTTCA TAGAGGAGCCAGATGATGCTTTATATCAAGAGCAACCTATTG 254

Qy 215 CACTCAGGTGCAAAAGCGAGCCAGCCATGCAGATATTTCTTCAATGCAACGCGAGTGGG 274

Db 255 CACTCAGGTGCAAAAGCGAGCCAGCCATGCAGATATTTCTTCAATGCAACGCGAGTGGG 314

Qy 275 TCATCAGAAAGCAGCAGCTCTCTGAAGAGACTCTGACGAGAGCTCAGTTTGAAGTCC 334

Db 315 TCATCAGAAAGCAGCAGCTCTCTGAAGAGACTCTGACGAGAGCTCAGTTTGAAGTCC 374

Qy 335 GCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGAGGACTTCCATGGGCCCGAGGACT 394

Db 375 GCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGAGGACTTCCATGGGCCCGAGGACT 434

Qy 395 ATTGGTCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAGAGCAGGAAGCCCTCTG 454

Db 435 ATTGGTCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAGAGCAGGAAGCCCTCTG 494

Qy 455 TGGCGATAGCCTATTACCGGAAAAAATTTTGAACAAGACCCCAAGGAAGGAAGTTCCCA 514

Db 495 TGGCGATAGCCTATTACCGGAAAAAATTTTGAACAAGACCCCAAGGAAGGAAGTTCCCA 554

Qy 515 TTGAAGGCATGATTGTTACTGCTGCGGCCCAACAGAGGAGTCCCTGCTGCCGAGTGG 574

Db 555 TTGAAGGCATGATTGTTACTGCTGCGGCCCAACAGAGGAGTCCCTGCTGCCGAGTGG 614

Qy 575 AATGCTGAAAAATGAAGAGCCCATTTGACTCTGAAACAAGACGAGAAACATTGACACAGGG 634

Db 615 AATGCTGAAAAATGAAGAGCCCATTTGACTCTGAAACAAGACGAGAAACATTGACACAGGG 674

Qy 635 CTGACCAATAACCTGATCATCAGGCAAGGCAAGGCTCTCGGACTCAGGAAATTAACCTGCA 694

Db 675 CTGACCAATAACCTGATCATCAGGCAAGGCAAGGCTCTCGGACTCAGGAAATTAACCTGCA 734

Qy 695 TGGCAGCCAAACATCGTGGCTTAAGAGAGAGGAGGCTGTCGCCCACTGTTGTTGTTAC 750

Db 735 TGGCAGCCAAACATCGTGGCTTAAGAGAGAGGAGGCTGTCGCCCACTGTTGTTGTTAC 794

Qy 751 ----- 750

Db 795 ATGGAGGCTGGTCTTCTTCTGGAAGAGTGGTCCAGCTGCAATGTTCTGCTGTGGTAGAGAT 854

Qy 751 ----- 750

Db 855 GGCAGAAAGCTTCCCGAGCTGCAACCAACCCAGCTCTCTCAATGTGGGGCCCTTTTGTG 914

Qy 751 -----GTGGATGGGAGCTGGG 766

Db 915 AGGGAATGTCAGTGCAGAAAAATAA CCTGCACTCTCTTTGCTCTGAGTGGGAGCTGGG 974

Qy 767 AAGTGTGAGCGCAATGGTCCGCTCTGCAAGTGTGAAACATTTGCGGATCCCGGAGT 826

Db 975 AAGTGTGAGCGCAATGGTCCGCTCTGCAAGTGTGAAACATTTGCGGATCCCGGAGT 1034

Qy 827 GCAAGCACAACCCCGAGAAATGGGGCAAAATTTCTGTAAGAGTCTAAGCCAGGAATCTG 886

Db 1035 GCAAGCACAACCCCGAGAAATGGGGCAAAATTTCTGTAAGAGTCTAAGCCAGGAATCTG 1094

Qy 887 AAAAATGCAAGATGGTCTTTCATCTAGATAAAAAA CTTCTTCATGAATAAAAAACCC 946

Db 1095 AAAAATGCAAGATGGTCTTTCATCTAGATAAAAAA CTTCTTCATGAATAAAAAACCC 1154

Qy 947 AAAGCAATTCAGAAATGCGAGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1006

Db 1155 AAAGCAATTCAGAAATGCGAGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1214

Qy	1007	CCGTTGCAGTCCTGGTCATTTGGTGTCAACCTTTTACAGACGGAGCCAGATGTACTATGGCG	1066
Db	1215	CCGTTGCAGTCCTGGTCATTTGGTGTCAACCTTTTACAGACGGAGCCAGATGTACTATGGCG	1274
Qy	1067	TGGACGTCATTGTACTCTTCTGCATTTGACAGGTGGCTTCCAGAGCTTCAACTTTCAAAACAG	1126
Db	1275	TGGACGTCATTGTACTCTTCTGCATTTGACAGGTGGCTTCCAGAGCTTCAACTTTCAAAACAG	1334
Qy	1127	TCGGTCAAGCCAAAGATATCATGGAACCTAATGATCAAGAAAATCTCTTTGGTAACTCCC	1186
Db	1335	TCGGTCAA-----GGTAACTCCC	1352
Qy	1187	TGCTCTGTAATTTCTGCCATCGACGCAGATCTGACAGTGAGCCGGAATACAGCGGAGCCCA	1246
Db	1353	TGCTCTGTAATTTCTGCCATCGACGCAGATCTGACAGTGAGCCGGAATACAGCGGAGCCCA	1412
Qy	1247	TCGTCTGCAGGACCTCTCTGGAACAAGAGCTCATGACAGAGTCCTCATCTCTTTAAACCTTT	1306
Db	1413	TCGTCTGCAGGACCTCTCTGGAACAAGAGCTCATGACAGAGTCCTCATCTCTTTAAACCTTT	1472
Qy	1307	TGTCGGACATCAAAGTGAAGTCCAGAGTCGTTCATTTGGTTCCCTGGAGTGTCTTGAGA	1366
Db	1473	TGTCGGACATCAAAGTGAAGTCCAGAGTCGTTCATTTGGTTCCCTGGAGTGTCTTGAGA	1532
Qy	1367	GAGCTGAGTACCGGCAAGATCATTTCCAGGACTTTTCCCATGGAACAACAACACAGCT	1426
Db	1533	GAGCTGAGTACCGGCAAGATCATTTCCAGGACTTTTCCCATGGAACAACAACACAGCT	1592
Qy	1427	TTAGTACAATGTCATCCAGAAATAAATGCCCTACATCCAAAATCTGTCACTACCTCCCA	1486
Db	1593	TTAGTACAATGTCATCCAGAAATAAATGCCCTACATCCAAAATCTGTCACTACCTCCCA	1652
Qy	1487	CAAGGACAGAACTGAGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGC	1546
Db	1653	CAAGGACAGAACTGAGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGC	1712
Qy	1547	CAAAATACAGGGGTGAGCTTACTCATACCAACACGGTGCCTCCAGAGGAGAAATCTTGGG	1606
Db	1713	CAAAATACAGGGGTGAGCTTACTCATACCAACACGGTGCCTCCAGAGGAGAAATCTTGGG	1772
Qy	1607	AGATTTATATGTCCATCAAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGC	1666
Db	1773	AGATTTATATGTCCATCAAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGC	1832
Qy	1667	TCCTGAGTCCTGAAGTCAACCTGTGGTCTCTCAGACATGATCGTCAACCTCTTGGCAT	1726
Db	1833	TCCTGAGTCCTGAAGTCAACCTGTGGTCTCTCAGACATGATCGTCAACCTCTTGGCAT	1892
Qy	1727	TGACCATCCCCGCACTGTGCAAGATGTCAAGTTCTGAGCAATTTGGAATATCCATTTAAAGAGA	1786
Db	1893	TGACCATCCCCGCACTGTGCAAGATGTCAAGTTCTGAGCAATTTGGAATATCCATTTAAAGAGA	1952
Qy	1787	GGACACACAGGGCAATGGGAGGAAGTGATGTCCAGTGGGAAGATGAACTTCACTCTGTT	1846
Db	1953	GGACACACAGGGCAATGGGAGGAAGTGATGTCCAGTGGGAAGATGAACTTCACTCTGTT	2012
Qy	1847	ACTGCTTTTGGACCCCTTTTGGTGTCAATGTGCTCTTGGAACGCTTTGGACCTATGCGC	1906
Db	2013	ACTGCTTTTGGACCCCTTTTGGTGTCAATGTGCTCTTGGAACGCTTTGGACCTATGCGC	2072
Qy	1907	TCACCTGGAGAGCCATCACAGACTGTGCCGTGAAGCAACTGAGGTGGCGTTTTTGGCT	1966
Db	2073	TCACCTGGAGAGCCATCACAGACTGTGCCGTGAAGCAACTGAGGTGGCGTTTTTGGCT	2132
Qy	1967	GCAATGCTCTAACTCCCTGGATTAACACTTTGAGAGTTTACTGTGTGGACAATAACCTTT	2026
Db	2133	GCAATGCTCTGTAACCTCCCTGGATTAACACTTTGAGAGTTTACTGTGTGGACAATAACCTTT	2192
Qy	2027	GTGCATTTTCAGGAAGTGGTTTTTCAGATGAAAGGCACTCAAGTGGACAGCTCTCTGGAAGAC	2086
Db	2193	GTGCATTTTCAGGAAGTGGTTTTTCAGATGAAAGGCACTCAAGTGGACAGCTCTCTGGAAGAC	2252
Qy	2087	CAAAAATGCTGCATTTCAAAGGGGAATACCTTTAGTCTTTTCAGATTTCTGTCTCTGATATTC	2146

Db	2253	CAAAATTTGCTGCATTTCAAAGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTC	2312
Qy	2147	CCCATTTCTCTGGAGAAATTAACCAATTCAC TGCCCTGCCAGAAAGTCCGGTTCTCCCGG	2206
Db	2313	CCCATTTCTCTGGAGAAATTAACCAATTCAC TGCCCTGCCAGAAAGTCCGGTTCTCCCGG	2372
Qy	2207	TGTGTTGCAGTAACCGGAGCCCTGCATGTGTGCCCTTCTCCCTGGAGCGTTATAGCCCA	2266
Db	2373	TGTGTTGCAGTAACCGGAGCCCTGCATGTGTGCCCTTCTCCCTGGAGCGTTATAGCCCA	2432
Qy	2267	CTACCAACCCAGCTGTCTCTGAAAATCTGCATTTCCGCGAGCTCAAAGCCATGAACAGATCC	2326
Db	2433	CTACCAACCCAGCTGTCTCTGAAAATCTGCATTTCCGCGAGCTCAAAGCCATGAACAGATCC	2492
Qy	2327	TCCAAGTGCAGACATCAATTCCTAGAGAGTGAACGAGAAACCATTCATTTCTTCGCAACAAG	2386
Db	2493	TCCAAGTGCAGACATCAATTCCTAGAGAGTGAACGAGAAACCATTCATTTCTTCGCAACAAG	2552
Qy	2387	AGGACAGCACTTTTCCTCTGCACAGACTGGGCCCAAAAGCCTTTCAAAATTTCCCTACTCCATCA	2446
Db	2553	AGGACAGCACTTTTCCTCTGCACAGACTGGGCCCAAAAGCCTTTCAAAATTTCCCTACTCCATCA	2612
Qy	2447	GACAGCGGATTTGTGCTACATTTTGATACCCCAATGCCAAAGCGCAGGACTGCGAGATGT	2506
Db	2613	GACAGCGGATTTGTGCTACATTTTGATACCCCAATGCCAAAGCGCAGGACTGCGAGATGT	2672
Qy	2507	TAGCACAGAAAAACAGCATCAACAGGAATTTATCTTTATTTTCGCTACACAAAGTAGCCCAT	2566
Db	2673	TAGCACAGAAAAACAGCATCAACAGGAATTTATCTTTATTTTCGCTACACAAAGTAGCCCAT	2732
Qy	2567	CTGTGTCTATTTTGAACCTGTGGGAAGCTCGTTCATCAGCATGTAGTGTGATCTTTGACTCCC	2626
Db	2733	CTGTGTCTATTTTGAACCTGTGGGAAGCTCGTTCATCAGCATGTAGTGTGATCTTTGACTCCC	2792
Qy	2627	TGGCTGTGCCCCTTTGAAGAGATTTGGGAGGACACACAGCAAACTCTCAAAATTTCAAGAT	2686
Db	2793	TGGCTGTGCCCCTTTGAAGAGATTTGGGAGGACACACAGCAAACTCTCAAAATTTCAAGAT	2852
Qy	2687	CCGAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGCACTCTAG	2736
Db	2853	CCGAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGCACTCTAG	2902

## RESULT 4

Accession #	LOCUS	DEFINITION	AX8000719	2868 bp	DNA	linear	PAT 13-OCT-2003
AF030221.1	LOCUS	Sequence 55 from Patent WO03055915.	AX8000719	2868 bp	DNA	linear	PAT 13-OCT-2003

**DEFINITION**  
**ACCESSION**

ACCESSION  
VERSION

## KEYWORDS

**SOURCE**

ORGANISM

**REFERENCE**

## REFERENCE

AUTHORS	TITLE
...	...

JOURNAL

## FEATURES

**sources**

## ORIGIN

11

Query Ma

Best Loc  
Matches

## Matches

8

3



Db 144 AGGAATGACAAATGGCGAGCCCTTCCCGAATCCATCCATCAGCTCCTGGGACACTGCC 203  
Qy 162 TCATTTTCATAGAGAGCCAGATGCTTATATATCAAGAGCAACCTTATGCACTCAG 221  
Db 204 TCATTTTCATAGAGAGCCAGATGCTTATATATCAAGAGCAACCTTATGCACTCAG 263  
Qy 222 GTCCAAAGCGAGGCCAGCCATGAGATATCTTCAAAATGCAACGGCGAGTGGGTCCATCA 281  
Db 264 GTCCAAAGCGAGGCCAGCCATGAGATATCTTCAAAATGCAACGGCGAGTGGGTCCATCA 323  
Qy 282 GAAACGAGCAGCTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCAAGT 341  
Db 324 GAAACGAGCAGCTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCAAGT 383  
Qy 342 GTTTCATCAATGTTACTAGGCAACAGGTGGAGAGCTTCCATGGGCCCGAGAGCTATTTGGTG 401  
Db 384 GTTTCATCAATGTTACTAGGCAACAGGTGGAGAGCTTCCATGGGCCCGAGAGCTATTTGGTG 443  
Qy 402 CCAGTGTGGTGGTGGAGCCACCTGGGTACCTCCAGAGCAGGAAAGGCTCTGTGGCAT 461  
Db 444 CCAGTGTGGTGGTGGAGCCACCTGGGTACCTCCAGAGCAGGAAAGGCTCTGTGGCAT 503  
Qy 462 AGCCTATTTACGGAAAACTTTGAAACAAGACCACCAAGGAAGGAAAGTTCCCAATTGAAGG 521  
Db 504 AGCCTATTTACGGAAAACTTTGAAACAAGACCACCAAGGAAGGAAAGTTCCCAATTGAAGG 563  
Qy 522 CATGATGTACTGCACTGCGGCCACACAGAGGAGTCCCTGTGCGAGGTGGAATGGCT 581  
Db 564 CATGATGTACTGCACTGCGGCCACACAGAGGAGTCCCTGTGCGAGGTGGAATGGCT 623  
Qy 582 GAAAAATGAAGAGCCCAATGACTCTGAAACAAGACGAGAACATTTGACACAGGCGCTGACCA 641  
Db 624 GAAAAATGAAGAGCCCAATGACTCTGAAACAAGACGAGAACATTTGACACAGGCGCTGACCA 683  
Qy 642 TAACTCTGATCATCAGGAGGACCGCTCTCGGACTCAGGAAATTTACACCTGCAATGGCAGC 701  
Db 684 TAACTCTGATCATCAGGAGGACCGCTCTCGGACTCAGGAAATTTACACCTGCAATGGCAGC 743  
Qy 702 CAACATCGTGGCTAAGAGGAGAAAGCTGTGCGGCACTGTGTGGTCTAC 750  
Db 744 CAACATCGTGGCTAAGAGGAGAAAGCTGTGCGGCACTGTGTGGTCTAC 803  
Qy 751 ----- 750  
Db 804 CTGGTCTTCTGACACAGAGTGGTCAGCTGCAATGTCGTTGGTGGTAGAGATGGCAGAA 863  
Qy 751 ----- 750  
Db 864 ACCTTCCCGGACCTGCACCAACCCAGCTCTCTCAATGGTGGGGCCCTTTTGTGAGGGAAT 923  
Qy 751 ----- GTGGATGGGAGCTGGGAAGTGTG 773  
Db 924 GTCAGTGCAGAAAAATAACCTGCACCTCTCTTTGCTGCTGGATGGGAGCTGGGAAGTGTG 983  
Qy 774 GAGCGAATGGTCCGTCTGCAAGTCCAGAGTGAACATTTGCGGATCCGGAGTGCACAGC 833  
Db 984 GAGCGAATGGTCCGTCTGCAAGTCCAGAGTGAACATTTGCGGATCCGGAGTGCACAGC 1043  
Qy 834 ACCACCCCGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAATCTGAAACTG 893  
Db 1044 ACCACCCCGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAATCTGAAACTG 1103  
Qy 894 CACAGATGGTCTTTGTCATCTAGATAAAAAACCTCTTTCATGAAATAAAAACCCCAAGCAT 953  
Db 1104 CACAGATGGTCTTTGTCATCTAG -----GCAT 1130  
Qy 954 TGAGATGCCAGGACATTTGCTTTGTACTCGGGCTTGGGTGCTGCCGTGTGGCCCTTGC 1013  
Db 1131 TGAGAATGCCAGGACATTTGCTTTGTACTCGGGCTTGGGTGCTGCCGTGTGGCCCTTGC 1190  
Qy 1014 AGTCTCTGGTCAATTTGGTGTCACTTACAGACGGAGCCAGAGTACTATGGCGTGGACGT 1073  
Db 1191 AGTCTCTGGTCAATTTGGTGTCACTTACAGACGGAGCCAGAGTACTATGGCGTGGACGT 1250

Qy 1074 CATTGACTCTTCTGCAATTTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCA 1133  
Db 1251 CATTGACTCTTCTGCAATTTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCA 1310  
Qy 1134 AGCCAAAGATATCATGGAACTAATGATACAAGAAAAATCCTTTTGGTAACTCCCTGTCTCCT 1193  
Db 1311 A -----GGTAACTCCCTGTCTCCT 1328  
Qy 1194 GAAATCTGCCATGCGACCGACAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCT 1253  
Db 1329 GAAATCTGCCATGCGACCGACAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCT 1388  
Qy 1254 GAGGAACTCTTGGAACAAGAGCTCATGACAGAGTCTCTCACTCTTTAAACCTTTGTGCGA 1313  
Db 1389 GCAGGACCTCTTGGAACAAGAGCTCATGACAGAGTCTCTCACTCTTTAAACCTTTGTGCGA 1448  
Qy 1314 CATCAAAGTGAAGTCCAGAGCTCGTTCATGTTTCCCTGGGAGTCTCTGAGAGAGCTGA 1373  
Db 1449 CATCAAAGTGAAGTCCAGAGCTCGTTCATGTTTCCCTGGGAGTCTCTGAGAGAGCTGA 1508  
Qy 1374 GTACCAAGGCAAGAAATCATTTCCAGAGCTTTTCCCAATGGAACAACACACAGCTTTAGTAC 1433  
Db 1509 GTACCAAGGCAAGAAATCATTTCCAGAGCTTTTCCCAATGGAACAACACACAGCTTTAGTAC 1568  
Qy 1434 AATGCAATCCAGAAATATAAATGCTTATCAATCAAAATCTGTATCATCTCCCAACAGGAC 1493  
Db 1569 AATGCAATCCAGAAATATAAATGCTTATCAATCAAAATCTGTATCATCTCCCAACAGGAC 1628  
Qy 1494 AGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAACTAGTAACTCAAAATAC 1553  
Db 1629 AGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAACTAGTAACTCAAAATAC 1588  
Qy 1554 AGGGGTGAGCTTACTCATACCAACGCTGCCATCCAGAGGAGAAATTTCTTGGAGATTTA 1613  
Db 1689 AGGGGTGAGCTTACTCATACCAACGCTGCCATCCAGAGGAGAAATTTCTTGGAGATTTA 1748  
Qy 1614 TATGTCATCAACCAAGGTGAACCCAGCTCCAGTCCAGATGGCTCTGAGGTCTCTGAG 1673  
Db 1749 TATGTCATCAACCAAGGTGAACCCAGCTCCAGTCCAGATGGCTCTGAGGTCTCTGAG 1808  
Qy 1674 TCTGAAGTCACTGTGGTCTCCAGACATGATCGTCAACACCTCCCTTTGCAATGGACCAT 1733  
Db 1809 TCTGAAGTCACTGTGGTCTCCAGACATGATCGTCAACACCTCCCTTTGCAATGGACCAT 1868  
Qy 1734 CCGCACTGTGCAGATGTCTGAGCAATTTGGAATATCCATTTAAAGAGAGGACACA 1793  
Db 1869 CCGCACTGTGCAGATGTCTGAGCAATTTGGAATATCCATTTAAAGAGAGGACACA 1928  
Qy 1794 GCAGGCAAAATGGAGGAGATGATGTCACTGAGAGATGAATCTACATCTGTTACTGCTT 1853  
Db 1929 GCAGGCAAAATGGAGGAGATGATGTCACTGAGAGATGAATCTACATCTGTTACTGCTT 1988  
Qy 1854 TTTGGACCCCTTTGGCGTGCATGTGCTCTTGACACCTTTGGACCTCTATGCGCTCACTGG 1913  
Db 1989 TTTGGACCCCTTTGGCGTGCATGTGCTCTTGACACCTTTGGACCTCTATGCGCTCACTGG 2048  
Qy 1914 AGAGCCAAATCACAGACTGTGCCGTGAAGCAACTGAAGTGGCGGTTTTTGGCTGCAATGC 1973  
Db 2049 AGAGCCAAATCACAGACTGTGCCGTGAAGCAACTGAAGTGGCGGTTTTTGGCTGCAATGC 2108  
Qy 1974 CTGTAACTCCCTGGATTAACAATTGAGAGTTTACTGTGTGGAACAATACCCCTTGTGCAAT 2033  
Db 2109 CTGTAACTCCCTGGATTAACAATTGAGAGTTTACTGTGTGGAACAATACCCCTTGTGCAAT 2168  
Qy 2034 TCAGGAAGTGGTTTTAGATGAAGGATCAAGGTGGACAGCTCTCGAGAGAACCAAAAT 2093  
Db 2169 TCAGGAAGTGGTTTTAGATGAAGGATCAAGGTGGACAGCTCTCGAGAGAACCAAAAT 2228  
Qy 2094 GCTGCAATTTCAAGGGAATACCTTTAGTCTTCAAGATTTCTGTCTTGTATATCCCCCAT 2153  
Db 2229 GCTGCAATTTCAAGGGAATACCTTTAGTCTTCAAGATTTCTGTCTTGTATATCCCCCAT 2288

QY	2154	CCTCTGAGAAATTAACCAATCACTGCTGCGCAGGAAGTCCCGTCTCCCGGTGGTG	2213	Db	61	GATCCTTATATATCAAGCAACCCCTATTGCACTAGGTGCAAGCGAGCCAGCCATG	120
Db	2289	CCTCTGAGAAATTAACCAATCACTGCTGCGCAGGAAGTCCCGTCTCCCGGTGGTG	2348	QY	244	CAGATATCTTCAAAATGCAACCGGAGTGGTTCATCAGAACGAGCAAGTCTCTGAGAG	303
QY	2214	CAGTAACGGCAGCCCTCGCACTGCTCTCCCTGAGCGTATATAGCCCACTACCAC	2273	Db	121	CAGATAATCTCAAAATGCAACCGGAGTGGTTCATCAGAACGAGCAAGTCTCTGAGAG	180
Db	2349	CAGTAACGGCAGCCCTCGCACTGCTCTCCCTGAGCGTATATAGCCCACTACCAC	2408	QY	304	ACTCTGAGCAGAGCTCAGGTTTGAAGTCCGGAAGTGTTCATCAATGTTACTAGGCAA	363
QY	2274	CCAGCTGTCTGCAAAATCTGCAATCGCAGAGTCAAAAGGCCATGAAAGTCTCAAGT	2333	Db	181	ACTCTGAGCAGAGCTCAGGTTTGAAGTCCGGAAGTGTTCATCAATGTTACTAGGCAA	240
Db	2409	CCAGCTGTCTGCAAAATCTGCAATCGCAGAGTCAAAAGGCCATGAAAGTCTCAAGT	2468	QY	364	CAGGTGAGAGACTTCCATGCGCCCGAGGACTATTGTTGTCAGTGTGTGGGTGAGCCAC	423
QY	2334	GCAGACATCAATCCTAGAGAGTGAACGAGAACCATCACTTTCTTCCGCAAGAGGACAG	2393	Db	241	CAGGTGAGAGACTTCCATGCGCCCGAGGACTATTGTTGTCAGTGTGTGGGTGAGCCAC	300
Db	2469	GCAGACATCAATCCTAGAGAGTGAACGAGAACCATCACTTTCTTCCGCAAGAGGACAG	2528	QY	424	CTGGTACTCTCAAGAGCAGGAAGCCCTCTGTGGCATAGCTATTTACGGAAACCTTT	483
QY	2394	CACCTTCCCTGACAGAGTGGCCCAAGCCTTCAAAATTCCTACTCCATCAGACAGCG	2453	Db	301	CTGGTACTCTCAAGAGCAGGAAGCCCTCTGTGGCATAGCTATTTACGGAAACCTTT	360
Db	2529	CACCTTCCCTGACAGAGTGGCCCAAGCCTTCAAAATTCCTACTCCATCAGACAGCG	2588	QY	484	GAAACAAGACCCACAAGGAAGGAAATGCCATTTGAAGGCATGATTTGTACTGCACTGCGC	543
QY	2454	GATTTGTGCTACATTTGATACCCCAATGCAAGCAAGGACTGGCAGATGTTAGCACA	2513	Db	361	GAAACAAGACCCACAAGGAAGGAAATGCCATTTGAAGGCATGATTTGTACTGCACTGCGC	420
Db	2589	GATTTGTGCTACATTTGATACCCCAATGCAAGCAAGGACTGGCAGATGTTAGCACA	2648	QY	544	CCACAGAGGAGTCCCTGTGCGGAGTGGAAATGGCTGAAAATGAAGGCCCATTTGAC	603
QY	2514	GAAACAGAGCATCAACAGGAATTTATCTTTATTTGCTACAGAGTAGCCATCTGCTGT	2573	Db	421	CCACAGAGGAGTCCCTGTGCGGAGTGGAAATGGCTGAAAATGAAGGCCCATTTGAC	480
Db	2649	GAAACAGAGCATCAACAGGAATTTATCTTTATTTGCTACAGAGTAGCCATCTGCTGT	2708	QY	604	TCTGAAACAGACGAGAACATTTGACACAGGCTGACCAATACCTGATCATCAGGAGGCA	663
QY	2574	CATTTTGAACCTGTGGAGCTGCTCATCAGCATGATGTTGATCTTGTACTCCCTGGCCTG	2633	Db	481	TCTGAAACAGACGAGAACATTTGACACAGGCTGACCAATACCTGATCATCAGGAGGCA	540
Db	2709	CATTTTGAACCTGTGGAGCTGCTCATCAGCATGATGTTGATCTTGTACTCCCTGGCCTG	2768	QY	664	CGGCTCTCGGACTCAGGAAATTTACACCTGATGCGAGCACAATCTGTGGCTTAAGAGAGA	723
QY	2634	TGCCCTTGAAGAGATGGGAGGACACACAGAACTCTCAAAATTTCAAGATCCAGCT	2693	Db	541	CGGCTCTCGGACTCAGGAAATTTACACCTGATGCGAGCACAATCTGTGGCTTAAGAGAGA	600
Db	2769	TGCCCTTGAAGAGATGGGAGGACACACAGAACTCTCAAAATTTCAAGATCCAGCT	2828	QY	724	AGCCTGTGCGGCACCTGTTGTGGTCTACGTAAGAGGCTGCTTCTCTGACAGAGTGG	660
QY	2694	TGATGAGCCGACTTCAACTACAGCAGCAAAATGGAATC	2733	Db	601	AGCCTGTGCGGCACCTGTTGTGGTCTACGTAAGAGGCTGCTTCTCTGACAGAGTGG	660
Db	2829	TGATGAGCCGACTTCAACTACAGCAGCAAAATGGAATC	2868	QY	751	-----	750
RESULT 5							
AX800717		2661 bp	DNA	linear	PAT 13-OCT-2003		
DEFINITION	Sequence 53 from Patent WO03055915.						
ACCESSION	AX800717						
VERSION	AX800717.1 GI:37653769						
KEYWORDS	Homo sapiens (human)						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	Fitzgerald, S.N., Fagan, R.J., Phelps, C.B., Power, C. and Yorke, M.						
AUTHORS	Fitzgerald, S.N., Fagan, R.J., Phelps, C.B., Power, C. and Yorke, M.						
TITLE	Transmembrane protein						
JOURNAL	Patent: WO 03055915-A 53 10-JUL-2003;						
FEATURES	AREP TRADING S.A. (CH) Location/Qualifiers 1..2661 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"						
ORIGIN	Query Match 81.1%; Score 2220; DB 6; Length 2661; Best Local Similarity 91.1%; Pred. No. 0; Matches 2493; Conservative 0; Mismatches 0; Indels 243; Gaps 3;						
QY	124	CTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCTCATTTTCATAGAGGAGCCAGAT	183	QY	1036	CTTTACAGCGGAGCAGAGTGAATGCGGTGGAGCTCATTTGACATCTTCTGCAATTTGACA	1095
Db	1	CTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCTCATTTTCATAGAGGAGCCAGAT	60	Db	1048	CTTTACAGCGGAGCAGAGTGAATGCGGTGGAGCTCATTTGACATCTTCTGCAATTTGACA	1107
QY	184	GATGCTTATATATCAAGAGCAACCCCTATTGCACTAGGTGCAAGGAGCCAGCCATG	243	QY	1096	GGTGGCTTCAGACCTTCAACTTTCAAAACAGTCCGTCGTAAGCCAGAAATATCATGGAAC	1155

Db 1108 GGTGGCTTCAGACCTTCAACTTCAAAAAGTCGGTCAA----- 1146  
Qy 1156 ATGATACAGAAAAATCTTTGGFACTCCCTGCTCTGTAATTCGCAATGACGACGAT 1215  
Db 1147 -----GGTAACTCCCTGCTCTGTAATTCGCAATGACGACGAT 1185  
Qy 1216 CTGACAGTGGCGGACATACAGCGACCATCTGCTGAGGACCCCTCTGGCAAGGAG 1275  
Db 1186 CTGACAGTGGCGGACATACAGCGACCATCTGCTGAGGACCCCTCTGGCAAGGAG 1245  
Qy 1276 CTGATGACAGAGCTCTCACTCTTTAAACCTTTTGGGACATCAAAAGTGAAGTCCAGAGC 1335  
Db 1246 CTGATGACAGAGCTCTCACTCTTTAAACCTTTTGGGACATCAAAAGTGAAGTCCAGAGC 1305  
Qy 1336 TCGTTGATGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAAGGCAAGATCAATCC 1395  
Db 1306 TCGTTGATGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAAGGCAAGATCAATCC 1365  
Qy 1396 AGGACTTTTCCCATGGAACAACCAAGCTTTAGTACAAATGATCCAGAAATAAATG 1455  
Db 1366 AGGACTTTTCCCATGGAACAACCAAGCTTTAGTACAAATGATCCAGAAATAAATG 1425  
Qy 1456 CCCTACATCCAAATCTGTCACTCCCAAGGACAGAACTGAGGACAACTGGTGTCT 1515  
Db 1426 CCCTACATCCAAATCTGTCACTCCCAAGGACAGAACTGAGGACAACTGGTGTCT 1485  
Qy 1516 TTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTATACCA 1575  
Db 1486 TTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTATACCA 1545  
Qy 1576 CAGGTGCCATCCAGAGGAGATTTCTGGAGATTTATATGTCATCAACCAAGGTGAA 1635  
Db 1546 CAGGTGCCATCCAGAGGAGATTTCTGGAGATTTATATGTCATCAACCAAGGTGAA 1605  
Qy 1636 CCCAGCTCCAGTCAGATGGCTCTGAGTGTCTCTGAGTCTCTGAAGTCACCTGTGTCT 1695  
Db 1606 CCCAGCTCCAGTCAGATGGCTCTGAGTGTCTCTGAGTCTCTGAGTCACCTGTGTCT 1665  
Qy 1696 CCAGACATGATGTGACCACTCCCTTTGCAATGACCAATCCGCACTGTGAGATGTCACT 1755  
Db 1666 CCAGACATGATGTGACCACTCCCTTTGCAATGACCAATCCGCACTGTGAGATGTCACT 1725  
Qy 1756 TCTGAGCATTTGAATATCCATTTAAAGAGAGACACAGAGGCAAAATGGGAGGAGTG 1815  
Db 1726 TCTGAGCATTTGAATATCCATTTAAAGAGAGACACAGAGGCAAAATGGGAGGAGTG 1785  
Qy 1816 ATGTGAGTGAAGATGAATCTACATCTCTGTTACTGCTTTTGGACCCCTTTGGTGTCT 1875  
Db 1786 ATGTGAGTGAAGATGAATCTACATCTCTGTTACTGCTTTTGGACCCCTTTGGTGTCT 1845  
Qy 1876 GTGCTCTGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCAATCAAGACTGTGCC 1935  
Db 1846 GTGCTCTGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCAATCAAGACTGTGCC 1905  
Qy 1936 GTGAGCACTGAAGTGGCGGTTTTTGGCTGATGTCGTGTAATCTCCCTGGATTAAC 1995  
Db 1906 GTGAGCACTGAAGTGGCGGTTTTTGGCTGATGTCGTGTAATCTCCCTGGATTAAC 1965  
Qy 1996 TTGAGAGTTTACTGTGTGGAACAATACCCCTTTGTGCAATTCAGGAAGTGGTTTCAGATGAA 2055  
Db 1966 TTGAGAGTTTACTGTGTGGAACAATACCCCTTTGTGCAATTCAGGAAGTGGTTTCAGATGAA 2025  
Qy 2056 AGGCATCAAGGTGGACAGCTCTCGGAAGAACCAAAATTCGTGCAATTCGAAGGGAATACC 2115  
Db 2026 AGGCATCAAGGTGGACAGCTCTCGGAAGAACCAAAATTCGTGCAATTCGAAGGGAATACC 2085  
Qy 2116 TTTAGTCTTCAGATTTTCTGCTTGTATATTCCTCCCATTCCTCTGGAGAAATTAACCATTC 2175  
Db 2086 TTTAGTCTTCAGATTTTCTGCTTGTATATTCCTCCCATTCCTCTGGAGAAATTAACCATTC 2145  
Qy 2176 ACTGCTTCGAGAGAGTCCGCTTCTCCGCGTGTGTGAGTAAACCGGAGCCCTGCGAC 2235  
Db 2146 ACTGCTTCGAGAGAGTCCGCTTCTCCGCGTGTGTGAGTAAACCGGAGCCCTGCGAC 2205

Qy 2236 TGTGCTTCTCCCTGGAGCGTTATACGCCCACTACCAACCCAGCTGTCTCTCAAAATCTGC 2295  
Db 2206 TGTGCTTCTCCCTGGAGCGTTATACGCCCACTACCAACCCAGCTGTCTCTCAAAATCTGC 2265  
Qy 2296 ATTGCGCAGCTCAAAAGCCATGAACAGATCCTCCAGTGCAGACATCAATCTCTAGAGAT 2355  
Db 2266 ATTGCGCAGCTCAAAAGCCATGAACAGATCCTCCAGTGCAGACATCAATCTCTAGAGAT 2325  
Qy 2356 GAACGAGAAACCATCACTTTTTCGACAGAGGACAGACATTTCCCTGACACAGACTGGC 2415  
Db 2326 GAACGAGAAACCATCACTTTTTCGACAGAGGACAGACATTTCCCTGACACAGACTGGC 2385  
Qy 2416 CCCAAAGCTTTCAAAATTTCCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACC 2475  
Db 2386 CCCAAAGCTTTCAAAATTTCCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACC 2445  
Qy 2476 CCCAATGCCAAAGGACGACTGGCAGATGTTAGCACAGAAAACAGACATCAACAGGAAT 2535  
Db 2446 CCCAATGCCAAAGGACGACTGGCAGATGTTAGCACAGAAAACAGACATCAACAGGAAT 2505  
Qy 2536 TTATCTTATTTTCGCTACAAAGTAGCCCATCTGCTGTCTCATTTTGAACCTGTGGAGCT 2595  
Db 2506 TTATCTTATTTTCGCTACAAAGTAGCCCATCTGCTGTCTCATTTTGAACCTGTGGAGCT 2565  
Qy 2596 CGTCATCAGCATGATGGTGTGATCTTGTACTCCCTGGCTGTGCCCTTGAAGAGATTGGAGG 2655  
Db 2566 CGTCATCAGCATGATGGTGTGATCTTGTACTCCCTGGCTGTGCCCTTGAAGAGATTGGAGG 2625  
Qy 2656 ACACACAGCAAACTCTCAACATTTTCAGATCCAG 2691  
Db 2626 ACACACAGCAAACTCTCAACATTTTCAGATCCAG 2661

RESULT 6  
MMU487854  
LOCUS  
DEFINITION  
Mus musculus mRNA for netrin receptor Unc5h4 (Unc5h4 gene).  
VERSION  
AJ487854.1 GI:22080675  
KEYWORDS  
netrin receptor Unc5h4; Unc5h4 gene.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

MMU487854 3925 bp mRNA linear ROD 24-SEP-2002  
Mus musculus mRNA for netrin receptor Unc5h4 (Unc5h4 gene).

netrin receptor Unc5h4; Unc5h4 gene.  
Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 Engelkamp, D.  
Cloning of three mouse unc-5 genes and their expression patterns at mid-gestation  
Unpublished  
REFERENCE  
2 (bases 1 to 3925)  
Engelkamp, D.  
Direct Submission  
Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for Brain Research, Deutscherordenstrasse 46, Frankfurt 60528, GERMANY  
Location/Qualifiers  
1. .3925  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
1. .3925  
/gene="Unc5h4"  
300. .3170  
/gene="Unc5h4"  
/codon\_start=1  
/product="netrin receptor Unc5h4"  
/protein\_id="CAD32252.1"  
/db\_xref="GI:22080675"  
/db\_xref="GOA:Q8K1S2"  
/db\_xref="UniProt/TrEMBL:O8K1S2"

FEATURES  
source  
1. .3925  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
1. .3925  
/gene="Unc5h4"  
300. .3170  
/gene="Unc5h4"  
/codon\_start=1  
/product="netrin receptor Unc5h4"  
/protein\_id="CAD32252.1"  
/db\_xref="GI:22080675"  
/db\_xref="GOA:Q8K1S2"  
/db\_xref="UniProt/TrEMBL:O8K1S2"

translation="MTGGAAGSRRRWLPWLGLFFWAGRAAARGADGSEILPDSI  
PSAPGTLPHFIEPEDAYIIKSNPIALRKARPMQIIFKNGEWHQNEHVEESLD  
ESSGLKRVREVFINVTRQVQEDFHPEDYWCQCVAMSHLGTGSKSRKASVRIAYLRKNFE

QDPQREVPIEGMIVLHCPPEGVPAAEVEMLKNEPIDSEODENIDTRADNHLIRQ  
ARLSDGNTICAAANIVAKRSLSATVYVYNGHNSWTESSACNVRGGRQKESRT  
CTNPAPLNGAFCEGNSVQKICTTALCPVDGSEWSEWSEVCSPECHRIJRECTAPP  
PRNGKFCGLSQESENCTDGLICILDKPLHEIKPFRWSRRRIENASDIALYSGUAP  
VAVAVLVGTLYRSHSDYDWDIDSSALTGGFTNFKTRQNSLLRNAMPQPD  
LTVSTVSGPI CLODPLDXELMTESLFPNLSDIKVKQSSPMVSLGVSERAEYHGKN  
HSGTFFHNNRGSSTHPRNKTPYIQLNLSLPRTELRTTGVFHLGRLVMPNTGVS  
LILPHGAIPEENSWIYMSINQSPSLQSDSEVLSPREVTGPPDMLVTPFPALTIP  
HCADVSSEHNHLKRTQGRWEVMSVEDSESTSCYCLLDPPFACHVLLDSFGTYALT  
GEPITDCAVKQLKAVFGCMNSLDYINLRVYCVNDTPCAQEVILSDERHGGQGLEE  
PKLLHFGKTFSLQVLDIPFLNRIKPTCAQEVFPFVSRWSSNRQPHQCAFSLRS  
TPPTTOLSKICITROLKHEQILOVOTSILESERETITPFAQEDSTFPQOTGPKAFKI  
PYSIRIICATPTDNAGKMDWMLAOKNSINRLSYFATQSSPSAVILNLEWRHQ  
DGLDLSACALBEIGRTHTKLSNITPEQIDADDNFYRQNGI"

ORIGIN

Query Match		72.5%;	Score 1982.6;	DB 10;	Length 3925;
Best Local Similarity		82.6%;	Pred. No. 0;		
Matches 2408;		Conservative 0;	Mismatches 284;	Indels 225;	Gaps 3;
Qy	3	GGGAGAGCGCGCGCCACCGCAGCGCGCGCGGAGGCGCGCGCTGGCTCCCGTGGCT	62		
Db	296	GAGCATGGGACAGGGGCTGCAGACGGCAGCCGCGGCGCGCGCTGCCATGGCT	355		
Qy	63	GGGCTGTGCTCTGGGCGCAGGACCGCGGCTGCCGAGGAACTGCAATGGCGAAGC	122		
Db	356	AGGACTCTTTTCTGGGCGCGGGGCTGGGCTGCCGAGGAGCCGATGGCAGTGAAT	415		
Qy	123	CTTTCGGAATCCATCCATCAGCTCCTGGGACACCTGCCTCATTTATNAGGAGCCAGA	182		
Db	416	TCTTCCGCACTCATCCCATCTGCCCTGGAACGCTGCCTCATTTTCATCGAGGAGCCGA	475		
Qy	183	TGATGCTATATATCAAGGACACCTATTGCACTCAGCTGCAAGGAGGCGACCCAT	242		
Db	476	AGATGCATACATCATCAAGGACACCCGATGTCATCAGTGCAAGGACGAGCCAGCCAT	535		
Qy	243	GCAGATATCTTCAAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGCTCTCTGAAGA	302		
Db	536	GCAGATCTTCTTCAAAATGCAATGGGAGTGGGTCCATCAGAAATGMAATGTGCGAGGA	595		
Qy	303	GACTCTGGAAGAGCTCAGGTTTGAAGGTCGCGGAGAGTCTTCAATGTTACTAGGCA	362		
Db	596	GAGCTTGGATGAGAGCTCAGGCTTGAAGGTCGCGGAGTGTATCAATGTACCCAGGCA	655		
Qy	363	ACAGTGGAGACTTCCATGGGCGCGAGGACTATTTGGTGCAGTGTGTGGCGTGGAGCCA	422		
Db	656	GCAAGTGGAGACTTCCATGGGCGCGAGGACTATTTGGTGCAGTGTGTGGCGTGGAGCCA	715		
Qy	423	CCTGGGTACTTCCAGAGCAGGAAGGCTCTGTGCGCATAGCCTATTTACGGAATACTT	482		
Db	716	CCTGGGAACGTCCAAGAGTAGGAAGGATCTGTGCGCATAGCCTATTTACGGAATACTT	775		
Qy	483	TGAACAGACCCACAGGAGGAGTTCCTTGAAGGAGATGTTACTGCACTGCCG	542		
Db	776	TGAACAGATCCAAGGAGGAGGTTTCTTATTTGAAGGAGATGATCGTGTGCTATGTCG	835		
Qy	543	CCACAGAGGAGTCCCTGTGCGCGAGGTGGATGGCTGAAAATGAAGGCCCATTTGA	602		
Db	836	CCCGCAGAGGAGTTCAGCAGCAGAGGTGGATGGCTGAAAATGAGGAGGCCATCGA	895		
Qy	603	CTCTGAAACAGACGAGAACTTGAACACAGGGCTGACCATTAACCTGATCATCAGGAGGC	662		
Db	896	CTCCGAAACAGGATGAGAACTTGAACACAGGGCTGACCATTAACCTGATCATCAGAGGC	955		
Qy	663	ACGGCTCTCGACTCAGGAATTAACCTGATGCGAGCCCAACATCTGGTGAAGAGAG	722		
Db	956	CCGGCTGTGAGACTCAGGAATTAACCTGATGCGAGCCCAACATCTGGTGAAGAGAG	1015		
Qy	723	AAGCTGTGCGGCACTGTGTGGTCTAC	750		
Db	1016	GAGCTCTCAGCAACTGTGGTGTCTACGTGAATGGAGGCTGTCTTCTCTGGACAGAGTG	1075		
Qy	751	-----	750		

Db	1076	GTCACGCTGCAATGTTCCCTGTGTGAGGATGCGAGAAAGCTTCCCGACCTGCACAA	1135		
Qy	751	-----	750		
Db	1136	CCCCGCTCTCTCAATGGTGGGGCCTTTTGTGAGGGAATGTCACTGCAGAAATAACCTG	1195		
Qy	751	-----GTGGATGGAGCTGGGAAGTGTGAGCGAAATGGTCCCTGTCTGAG	794		
Db	1196	CACCTGCTTTTGTCTCTGGATGGCAGCTGGGAAGTGTGAGTGAATGCTGCTGAG	1255		
Qy	795	TCCAGAGTGTGAACATTTTCCGGATCCGGAGTGCACAGCACCCCGGAGAAATGGGG	854		
Db	1256	CCCAGAGTGTGAACATCTTCTGATCCGATGTGCACAGCTCCACCCCAAGAAATGGGG	1315		
Qy	855	CAAAATCTGTCAAGCTTAAGCCAGGAATCTGAAAACTGCACAGATGCTTTTCATCTCT	914		
Db	1316	CAAGTTCTGTGAAGTCTCAGCCAGGAATCTGAAAACTGCACAGATGCTTCTGCAATCT	1375		
Qy	915	AGATAAAAAACCTCTTTCATGAAATAAAACCCCAA-----GCATTGAGAA	959		
Db	1376	AGATAAAAAACCTCTTTCATGAAATAAAACCCCAAAGATGGAGTAGGAGGCAATTGAGAA	1435		
Qy	960	TGCCAGCAGCAATTTGTTACTCGGCTTGGGTGCTGCGCTGCTGGCCGTTCAGATCT	1019		
Db	1436	TGCCAGCAGCAATTTGTTACTCGGCTTGGGTGCGCCGTGGTAGCTTTGGGTCT	1495		
Qy	1020	GGTCATTGGTGTACCCCTTTACAGACGGAGCCAGAGTGAATATGGCGTGGACGTCATTGA	1079		
Db	1496	GGTCATTGGTGTACCCCTTTACAGACGGAGCCACAGTGAATACGAGTGGATGTCAATGA	1555		
Qy	1080	CTCTTCTGCAATGACAGTGGCTTCCAGACCTTCAATTTCAAAACAGTCCCTCAAGCCAA	1139		
Db	1556	CTCTTCTGCAATGACAGTGGCTTCCAGACCTTCAATTTCAAAACAGTTCGTCAA-----	1610		
Qy	1140	GAATATCATGGAATTAATGATACAGAAAAATCTTTTGTGTAATCTCTTCTCTCTGAAATTC	1199		
Db	1611	-----GGAAATCTCTTCTTACTTGAATCC	1633		
Qy	1200	TGCCATGACGCCAGATCTGACAGTGAAGCGGACATACAGCGGACCCATCTGTCTGCAGGA	1259		
Db	1634	TGCCATGACGCCAGATCTGACAGTGAAGCGGACATACAGCGGCGCCATCTGTCTGCAGGA	1693		
Qy	1260	CCCTCTGACAGGAGCTCATGACAGAGTCCCTCACTTTAACTTCTTGTTCGAGCATCAA	1319		
Db	1694	TCCGTTCGACAGGAGCTCATGACAGAGTCCCTCACTTTCAATCTCTTATCTGACATCAA	1753		
Qy	1320	AGTGAAGTCCAGAGCTGTTTCAATGTTTCCCTGGGAGTGTCTGAGAGAGTGAATGCA	1379		
Db	1754	AGTGAAGTCCAGAGCTGTTTCAATGTTTCCCTGGGAGTGTCTGAGAGAGTGAATGCA	1813		
Qy	1380	CGGCAAGAAATCATTCAGGACTTTTCCCATGGAACCAACACAGCTTTAGTACAAATGCA	1439		
Db	1814	TGGCAAGAAATCATTCAGGACTTTTCCCATGGAACCAACCAACCGGAGTTCAGTACAAATGCA	1873		
Qy	1440	TCCAGAAATAAAATGSCCTTACATCCAAATCTGTCTCATCTCCCAACAGGACAGAACT	1499		
Db	1874	TCCAGAAATAAAATGSCCTTACATCCAAATCTGTCTCATCTCCCAACAGGACAGAGCT	1933		
Qy	1500	GAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCGCAAAATACAGGGGT	1559		
Db	1934	GAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCGCAAAATACAGGGGT	1993		
Qy	1560	GAGCTTACTCATACACAGTGGCCATCCAGAGGAGAAATCTTGGAGATTTATATGTC	1619		
Db	1994	GAGCTTACTCATACACAGTGGCCATCCAGAGGAGAAATCTTGGAGATTTATATGTC	2053		
Qy	1620	CATCAACCAAGGTGAACCCAGCCTCCAGTCAAGTGGCTCTGAGGTGCTCTGAGTCTCTGA	1679		
Db	2054	AATCAACCAAGGTGAACCCAGCCTCCAGTCAAGTGGCTCTGAGGTGCTCTGAGTCTCTGA	2113		
Qy	1680	AGTCACTGTGGTCTTCCAGACATGATCGTCAACCTCCCTTTGCAATGACCAATCCGCA	1739		

Db 2114 AGTCACCTGTGGGCTCCAGATATGCTTGTACACACTCCCTTTTGGCTGACCATCCCTCA 2173  
Qy 1740 CTGTGCAGATGTCAGTTCTGAGCAATGGAATATCATTAAAGAGAGGACACAGCAGGG 1799  
Db 2174 CTGTGCAGAGCTCAGTTCTGAGGACCTCGAACTTACCTGAGAGAGGACCCAGCAGGG 2233  
Qy 1800 CAAATGGAGAGTGTATGTCAGTGGAGATGAATCTACATCCTGTGTACCTTTTGGGA 1859  
Db 2234 GAAGTGGAGAGTGTATGTCAGTGGAGGATGATCCACATCCTGTGTACTGCTTTGGGA 2293  
Qy 1860 CCCCTTTGCGTGCATGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCC 1919  
Db 2294 TCCCTTTGCGTGCATGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCC 2353  
Qy 1920 AATCAGAGCTGCGCTGAGAGCACTGAAAGTGGCGGTTTGGCTGCAATGCTCTGTAA 1979  
Db 2354 AATCAGAGCTGCGCTGAGAGCACTGAAAGTGGCTGCTGTTGGCTGCAATGCTCTGTAA 2413  
Qy 1980 CTCCTCGATTACAACTTGGAGTTTACTGTGGACAATACCCCTGTGCAATTCAGGA 2039  
Db 2414 CTCCTCGATTACAACTTGGAGTTTACTGTGGACAATACCTTGTGCAATTCAGGA 2473  
Qy 2040 AGTGGTTTCAGATGAAGGATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTTGCTGCA 2099  
Db 2474 AGTGATTTCTGACGACGACCAAGGCGCCAGCTCCTGGAAGAACCAAAATTTGCTGCA 2533  
Qy 2100 TTTCAAAGGAATACCTTTAGTCTTCTGAGATTTCTGCTCTGTGATTTCCCTCCCTCTG 2159  
Db 2534 TTTCAAAGGAATACCTTTAGTCTTCTGAGATTTCTGCTCTGTGATTTCCCTCCCTCTG 2593  
Qy 2160 GAGATTTAAACCTTCACTGCTGCCAGGAGTCCCGTTCTCCGCGGTGGTGGCAGTAA 2219  
Db 2594 GAGATTTAAACCTTCACTGCTGCCAGGAGTCCCGTTCTCCGCGGTGGTGGCAGCAA 2653  
Qy 2220 CCGGACGCTGCACTGTGCTCTTCCCTGGAGCGTTTATACGCCACTACCAACCCAGCT 2279  
Db 2654 CCGGACGCTGCACTGTGCTCTTCCCTGGAGCGTTTATACGCCACTACCAACCCAGCT 2713  
Qy 2280 GTCTGCAAAATCTGCAATTCGGAGCTCAAGGCGATGAACAGATCTCAGAGTGGAGAC 2339  
Db 2714 GTCTGCAAAATCTGCAATTCGGAGCTCAAGGCGATGAACAGATCTCAGAGTGGAGAC 2773  
Qy 2340 ATCAATCTAGAGTGAAGCGAAGACCATCTCTTCTGCGCAAGAGGACGACCTTT 2399  
Db 2774 ATCAATCTAGAGTGAAGCGAAGACCATCTCTTCTGCGCAAGAGGACGACCTTT 2833  
Qy 2400 CCTGCAAGACTGGCCCTCAAGGCTTCAAAATTCCTTACTTCCATCAGACAGAGGATTTG 2459  
Db 2834 TCCTGCAAGACTGGCCCTCAAGGCTTCAAAATTCCTTACTTCCATCAGACAGAGGATTTG 2893  
Qy 2460 TGCTACATTTGATACCCCTCAAGGCTTCAAAATTCCTTACTTCCATCAGACAGAGGATTTG 2519  
Db 2894 CGCCACGTTTGTATACCCCTCAAGGCTTCAAAATTCCTTACTTCCATCAGACAGAGGATTTG 2953  
Qy 2520 CAGCATCAAGGATTTTATCTTCTGCTGACAGAGTGGCCCTTCCCTGCTGCTTTT 2579  
Db 2954 CAGCATCAAGGATTTTATCTTCTGCTGACAGAGTGGCCCTTCCCTGCTGCTTTT 3013  
Qy 2580 GAACCTGTGGAGAGCTGCTCATCAGCATGATGTGTGATCTTGAATCTTCCCTGCTGCTTT 2639  
Db 3014 GAACCTGTGGAGAGCTGCTCATCAGCATGATGTGTGATCTTGAATCTTCCCTGCTGCTTT 3073  
Qy 2640 TGAAGAGATTTGGAGGACACACAGAACTCTCAAACTTCAAGATTCAGATTCAGATTTGATGA 2699  
Db 3074 TGAAGAGATTTGGAGGACACACAGAACTCTCAAACTTCAAGATTCAGATTCAGATTTGATGA 3133  
Qy 2700 AGCGACTTCAACTACAGGAGGCAAAATGACTCTAG 2736  
Db 3134 TGCTGACTTCAACTACAGGAGGCAAAATGACTCTAG 3170

RESULT 7  
CQ841583

LOCUS CQ841583 2448 bp DNA linear PAT 02-AUG-2004  
DEFINITION Sequence 230 from Patent EPI440981.  
ACCESSION CQ841583  
VERSION CQ841583.1 GI:50893370  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Iehii,S.,  
Yamamoto,J., Isono,Y., Nagai,K. and Irie,R.  
TITLE Full-length human cdna  
JOURNAL Patent: EP 1440981-A 230 28-JUL-2004;  
Research Association for Biotechnology (JP)  
FEATURES  
Location/Qualifiers  
source 1..2448  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 58.5%; Score 1599.8; DB 6; Length 2448;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1601; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1134 AGCCAAAGATATCATGGAATATGATACAAAGAAAATCCTTTGGTAACTCCCTGCTCT 1193  
Db 99 AGCCAAAGATATCATGGAATATGATACAAAGAAAATCCTTTGGTAACTCCCTGCTCT 158  
Qy 1194 GAATTCCTCCATCGACCCAGATCTGACAGTGCAGGACATACAGCGGACCCATCTGCT 1253  
Db 159 GAATTCCTCCATCGACCCAGATCTGACAGTGCAGGACATACAGCGGACCCATCTGCT 218  
Qy 1254 GCAGGACCTCTCGCAAGAGGAGTCTATGACAGAGTCTCTCACTCTTTAAACCTTTGTCGA 1313  
Db 219 GCAGGACCTCTCGCAAGAGGAGTCTATGACAGAGTCTCTCACTCTTCAACCTTTGTCGA 278  
Qy 1314 CATCAAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGAGTGTCTGAGAGAGCTGA 1373  
Db 279 CATCAAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGAGTGTCTGAGAGAGCTGA 338  
Qy 1374 GTACCAAGGCAAGATCAATCCAGGACTTTTCCCATGGAACACACACAGCTTTAGTAC 1433  
Db 339 GTACCAAGGCAAGATCAATCCAGGACTTTTCCCATGGAACACACACAGCTTTAGTAC 398  
Qy 1434 AATGCATCCCAAGAAATAAATGCCATACATCCAAATCTCTCATCTCCCCCAAGGAC 1493  
Db 399 AATGCATCCCAAGAAATAAATGCCATACATCCAAATCTCTCATCTCCCCCAAGGAC 458  
Qy 1494 AGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATAC 1553  
Db 459 AGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATAC 518  
Qy 1554 AGGGGTGAGCTTACTCATACCAACGCTGCCATCCCAAGAGAGAAATCTTTGGGAGATTTA 1613  
Db 519 AGGGGTGAGCTTACTCATACCAACGCTGCCATCCCAAGAGAGAAATCTTTGGGAGATTTA 578  
Qy 1614 TATGTCCATCAACCAAGGTGAACCCAGCTCCAGTCCAGTCCAGTGGCTCTGAGGTGCTCTGAG 1673  
Db 579 TATGTCCATCAACCAAGGTGAACCCAGCTCCAGTCCAGTGGCTCTGAGGTGCTCTGAG 638  
Qy 1674 TCCTGAAGTCACTGTGGTCTCCAGACATGATGTCATCCATCCCTTTTGCATTGACCAT 1733  
Db 639 TCCTGAAGTCACTGTGGTCTCCAGACATGATGTCATCCATCCCTTTTGCATTGACCAT 698  
Qy 1734 CCGGCACTGTGAGAGTGTGAGTCTGAGCAATTCGGAATATCCATTAAGAGAGGACACA 1793  
Db 699 CCGGCACTGTGAGAGTGTGAGTCTGAGCAATTCGGAATATCCATTAAGAGAGGACACA 758  
Qy 1794 GCAGGGCAAAATGGGAGAGTGTGATGTCAGTGGAGAGTGAATCTACATCTCTGTTACTGCT 1853  
Db 759 GCAGGGCAAAATGGGAGAGTGTGATGTCAGTGGAGAGTGAATCTACATCTCTGTTACTGCT 818



1854 TTTGGACCCCTTTGGCTGTCATGCTCTCTGGACAGCTTTGGACCTATGCGCTCACTGG 1913  
 Db TTTGGACCCCTTTGGCTGTCATGCTCTCTGGACAGCTTTGGACCTATGCGCTCACTGG 878  
 1914 AGAGCCAATCACAGACTGTCCTGGAAGCACTGAAGTGGCGTTTGGTGGCATGTC 1973  
 Db TTTGGACCCCTTTGGCTGTCATGCTCTCTGGACAGCTTTGGACCTATGCGCTCACTGG 938  
 879 AGAGCCAATCACAGACTGTCCTGGAAGCACTGAAGTGGCGTTTGGTGGCATGTC 938  
 1974 CTGTAACTCCTCTGGATTACAACCTTGAGAGTTTACTGTGTGGCAATACCCCTTGTGCAT 2033  
 Db CTGTAACTCCTCTGGATTACAACCTTGAGAGTTTACTGTGTGGCAATACCCCTTGTGCAT 998  
 2034 TCAGGAAGTGGTTTCAGATGAAGGCACTCAAGTGCAGAGCTCTGGAGAACCAAAAT 2093  
 Db TCAGGAAGTGGTTTCAGATGAAGGCACTCAAGTGCAGAGCTCTGGAGAACCAAAAT 1058  
 2094 GCTGCATTTCAAAGGGAATACCTTTAGTCTTTCAGATTTCTGCTCTTGTATATCCCCCAT 2153  
 Db GCTGCATTTCAAAGGGAATACCTTTAGTCTTTCAGATTTCTGCTCTTGTATATCCCCCAT 1118  
 1059 GCTGCATTTCAAAGGGAATACCTTTAGTCTTTCAGATTTCTGCTCTTGTATATCCCCCAT 1118  
 2154 CTTCTGAGAAATTAACCAATCTCTGCTGCGAGGAGTCCCTTCTCCCGGTGGTG 2213  
 Db CTTCTGAGAAATTAACCAATCTCTGCTGCGAGGAGTCCCTTCTCCCGGTGGTG 1178  
 1119 CTTCTGAGAAATTAACCAATCTCTGCTGCGAGGAGTCCCTTCTCCCGGTGGTG 1178  
 2214 CAGTAACCGGCGAGCCCTGCACTGTGCTTCTCCCTGGAGCGTTATAGGCCACTACCAC 2273  
 Db CAGTAACCGGCGAGCCCTGCACTGTGCTTCTCCCTGGAGCGTTATAGGCCACTACCAC 1238  
 1179 CAGTAACCGGCGAGCCCTGCACTGTGCTTCTCCCTGGAGCGTTATAGGCCACTACCAC 1238  
 2274 CCAGCTCTCTGCAAAATCTGCAATCTGCGAGCTCAAGGCGCATGAACAGATCTCCAAGT 2333  
 Db CCAGCTCTCTGCAAAATCTGCAATCTGCGAGCTCAAGGCGCATGAACAGATCTCCAAGT 1298  
 2334 GCAGACATCAATCTAGAGAGTGAAACAGAAACCATCACTTTCTTGCCACAAGGACAG 2393  
 Db GCAGACATCAATCTAGAGAGTGAAACAGAAACCATCACTTTCTTGCCACAAGGACAG 1358  
 2394 CACTTTCCCTGACAGAGTGGCCCAAGGCTTCAAAATTCCTTACTTCCATCAGACAGCG 2453  
 Db CACTTTCCCTGACAGAGTGGCCCAAGGCTTCAAAATTCCTTACTTCCATCAGACAGCG 1418  
 2454 GATTGTGCTCAATTTGATACCCCAATGCAAGGCAAGGAGTGGAGATGTTAGACA 2513  
 Db GATTGTGCTCAATTTGATACCCCAATGCAAGGCAAGGAGTGGAGATGTTAGACA 1478  
 2514 GAAAAACAGCATCAACAGGAATTTATCTTATTTGCTTACCAAGTGGCCATCTGCTGT 2573  
 Db GAAAAACAGCATCAACAGGAATTTATCTTATTTGCTTACCAAGTGGCCATCTGCTGT 1538  
 2574 CATTTTGAACCTGTGGAGCTCGTCATCAGCATGATGTTGATCTTGACTCCCTGGCCTG 2633  
 Db CATTTTGAACCTGTGGAGCTCGTCATCAGCATGATGTTGATCTTGACTCCCTGGCCTG 1598  
 2634 TGCCCTTGAAGAGATTGGAGGACACACAGAACTCTCAAACTTCAGAAATCCAGCT 2693  
 Db TGCCCTTGAAGAGATTGGAGGACACACAGAACTCTCAAACTTCAGAAATCCAGCT 1658  
 2694 TGATGAGCCGACTTCACTACAGAGGCAAAATGGACTCTAG 2736  
 Db TGATGAGCCGACTTCACTACAGAGGCAAAATGGACTCTAG 1701

RESULT 8  
 AK122610  
 LOCUS Homo sapiens cDNA FLJ16019 fis, clone BRAM2001473, weakly similar  
 DEFINITION to Rattus norvegicus transmembrane receptor Unc5H2 mRNA.  
 ACCESSION AK122610  
 VERSION AK122610.1  
 KEYWORDS oligo capping; fis (full insert sequence).  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS

1 Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,  
 Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,  
 Otsuki T., Sato H., Wakatsuki A., Ishii S., Yamamoto J., Isono Y.,  
 Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
 Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
 Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A.,  
 Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S.,  
 Naganari K., Masuho Y., Nagai K. and Isogai T.  
 NEDO human cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 2448)

TITLE  
 JOURNAL

Isogai T. and Yamamoto J.  
 Direct Submission  
 Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7  
 Kase-Kamatari, Kisarazu, Chiba 292-0818, Japan  
 (E-mail: genomics@hri.co.jp, tel: 81-438-52-3975, fax: 81-438-52-3986)

AUTHORS  
 JOURNAL

NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction: Helix Research Institute (HRI) (supported by Japan  
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
 HRI, and Biotechnology Center, National Institute of Technology and  
 Evaluation; clone selection for full insert sequencing: HRI and  
 RAB; annotation: HRI and RAB.  
 Location/Qualifiers  
 1..2448  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="BRAMY2001473"  
 /tissue\_type="amygdala"  
 /clone\_lib="BRAMY2"  
 /note="cloning vector: pME18SFL3"

FEATURES  
 Source

1..2448  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="BRAMY2001473"  
 /tissue\_type="amygdala"  
 /clone\_lib="BRAMY2"  
 /note="cloning vector: pME18SFL3"

ORIGIN

Query Match 58.5%; Score 1599.8; DB 9; Length 2448;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1601; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1134 AGCCAGATATCATGGAACCTAATGATACAGAAAAATCTTTGGTAACCTCCTGCTCT 1193  
 Db 99 AGCCAGATATCATGGAACCTAATGATACAGAAAAATCTTTGGTAACCTCCTGCTCT 158  
 QY 1194 GAATTCCTGCGATCGACCCAGATCTGACAGTGGCGGCAATACAGCGGACCCATCTGCT 1253  
 Db 159 GAATTCCTGCGATCGACCCAGATCTGACAGTGGCGGCAATACAGCGGACCCATCTGCT 218  
 QY 1254 GCGAGCCCTCTGGCAAGGAGCTCATGACAGAGTCTTAACTTTTAACTTTGTCGA 1313  
 Db 219 GCGAGCCCTCTGGCAAGGAGCTCATGACAGAGTCTTAACTTTTAACTTTGTCGA 278  
 QY 1314 CATCAAGTGAAGTCCAGAGCTCGTTTATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 1373  
 Db 279 CATCAAGTGAAGTCCAGAGCTCGTTTATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 338  
 QY 1374 GTACCAAGGCAAGATCATTCAGAGCTTTTCCCATGGAACCAACCAAGCTTTAGTAC 1433  
 Db 339 GTACCAAGGCAAGATCATTCAGAGCTTTTCCCATGGAACCAACCAAGCTTTAGTAC 398  
 QY 1434 AATGCATCCAGAAATATAATGCCCTTACATCAAAATCTGTCTCACTCCCCCAAGGAC 1493  
 Db 399 AATGCATCCAGAAATATAATGCCCTTACATCAAAATCTGTCTCACTCCCCCAAGGAC 458  
 QY 1494 AGAAGTGGAGCAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTATGATGCAATATAC 1553  
 Db 459 AGAAGTGGAGCAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTATGATGCAATATAC 518  
 QY 1554 AGGGGTGAGCTTACTCATACCAAGCTGCCAGAGGAGAAATCTTTGGGAGATTTA 1613  
 Db 519 AGGGGTGAGCTTACTCATACCAAGCTGCCAGAGGAGAAATCTTTGGGAGATTTA 578

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.





Qy	659	AGGCACGGCTCTCGGACTCAGGAAATTTACACCTGCAATGCAGCACCACATCTGGTGAAGA	718
Db	626	AGSCCCGCTGTGGGACACTGCCAACTATACCTGTGCGTGCCAGAAACATCTGTGGCCAAAC	685
Qy	719	GGAGAAGCCCTGTGGGCCACTGTGTGGTCTACGTGATCG-----GAGCTGGGAAG	769
Db	686	GCCGGAGACCACTGGCCACCGTCATCGTCTACGTGAATGGCGCTGGTCCAGCTGGGCGAG	745
Qy	770	TGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGC	829
Db	746	AGTGGTCACTCTGCTCCAAACCGCTGTGGCGAGGCTGCGCAGAAGCGCACCGGACCTGCA	805
Qy	830	CAGCACCAACCCCGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAACTCTGAAA	889
Db	806	CCAAACCCGCTCCACTCAACCGAGGGGCGCTTCTGCGAGGGCCAGGCAATTCAGAGAAGCCG	865
Qy	890	ACTGCAACAGATGCTTTTGCATCCTAGATAAAAAACCTCTTCATGAATAAAAAACCCCAA	949
Db	866	CTTGCAACC-----ACCATCTGCCCGAG	886
Qy	950	GCAATGAGAAATCCAGCGACATTTGCTTTGTACTCGGCGTTGGGTGCTGCGCTCGTGCCG	1009
Db	887	TGCTGGAGGCTCAGGGGATCGCGCGCTGTATCGGGGCTCGTGTGTGGCCATCTTCGTG	946
Qy	1010	TTTCAG-----TCCTGGTCAATTTGGTGTACCCCTTTACAGACGGAGCCAGAGTGACTATG	1063
Db	947	TCGTGGCAATCTCTATCGCGGTGGGGTGTGTGTACCGCCCACTGCCGTGACTTCG	1006
Qy	1064	CGGTGGACGTCAATGACTCTTCT-----GCAATGACAGTGGCTTCCAGACCTTCAACTTCA	1120
Db	1007	ACACAGACATCACTGACTCATCTGTCTGCCCTGACTGTGTGTTTCCACCCCGTCAACTTTA	1066
Qy	1121	AAACAGTCCGTCAAGCCAGAAATCATGAGAACTAATGATACAGAAGAAATCCTTTGGTA	1180
Db	1067	AGACGGCAAGGC-----CCAGCA	1084
Qy	1181	ACTCCCTGCTCCTGAAATTCGCCATGCAGCCAGATCTGACAGTGAG---CCGACATACA	1237
Db	1085	ACCCGACGCTCTACACCCCTCTGTGCTCTGTACCTGACAGCGAGCGCGGCATCTACC	1144
Qy	1238	CGGACCCATCTGT---CTGAGAGCCCTCTGACAGAGAGCTCATGACAGAGTCTCTCAC	1294
Db	1145	CGGACCCGTTATGTCCTCGAGACTCCACCGCAAAATCCCCATGACCACTCTCCTC	1204
Qy	1295	TCCTTAACCTTTGTCGGAATCAAAAGTGAAGTCCAGAGCTGTTTCAATGGTTTC-----	1350
Db	1205	TGCTGGACCCCTTACCCAGCCTTAAGGTCAAGTCTACAGTCTCAGCACACCGGCTCTG	1264
Qy	1351	--CTGGAGTGTCTGAGAGAGCTGAGTACACAGCAAGATCATTCAGAGACTTTTCCCC	1408
Db	1265	GCCAGAGCTGGCAGATGGGCTGACCTGTGGGGGTCTTGCCGCGCTGGCACATACCCTA	1324
Qy	1409	ATGGAACAACACACAGCTTTAGTACAAATGCATCCAGAAATAAAATGCCCTACATCCAAA	1468
Db	1325	CGAATTTGCCCGGACACCACTTCCTGCACTGCGAGCGCCAGCTCGGTTCCGAGC	1384
Qy	1469	ATCTGTCACTACCTCCCAACAGGACAGAACTGAGGACAACTGTGTGCTTTGGGCCATTTAG	1528
Db	1385	AGCTCTTGGGCTGCCCCGAGACCCGAGGAGCAGCGTCAGCGGCACCTTTGGTGGCTCG	1444
Qy	1529	GGGGCGCTTAGTAATGCCAATACAGGGTGAGCTTACTCATACACAGGTGCCATCC	1588
Db	1445	GTGGAGGCTCAGCATCCCGGCAAGGGGTACGCTTGCTGGTGCCCAATGGAGCCATTC	1504
Qy	1589	CAGAGGAGAAATCTTTGGGAGATTTATATGTCATCAACCAAGGTGAACCCAGCTCCAG-	1647
Db	1505	CCAGGGCAAGTCTCTCAGATGTATCTACTCATCAACAGGCGAGAAAGTACCTCCCGC	1564
Qy	1648	--TCAGATGGCTCTGAGGTGCTCTGAGTCTCTGAGTCTGTAAGTCACTGTGTCTTCCAGACATGA	1705
Db	1565	TTTTCAGAGGGAACCAAGACAGTATTGAGCCCTCGGTGACTGTGGACCCACAGGCTTC	1624
Qy	1706	TCGTCAACACTCCCTTTTGCAATTTGACCAATCCCGCACTGTGCAGATGTCTAGTTCTGAGCATT	1765

Db	1625	TGCTGTGCGCCCGTCATCCTCACATGCGCCACATGTGCGCGAGTGCAGTGCCTGACT	1684
Qy	1766	GGAAATATCCATTTAAAGAAAGAGACACAGCAGGGCAAATGGAGGAAGTGAATGTCAATGG	1825
Db	1685	GGATCTTTAGCTCAAGACCAGGCCCAACAGGGCCACTGGAGGAGGTGGTGAACCTGG	1744
Qy	1826	AAGATGAATCT-----ACATCTGTGTACTGCTTTTGACCCCTTTGCTGTGTCATGTGC	1879
Db	1745	ATGAGGAGACCTTGAACACACACCCCTGTACTGCGCAGCTGGAGCCAGGGCTGTGCATCTC	1804
Qy	1880	TCTTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCAAATCACAGACTGTGCGCGTGA	1939
Db	1805	TGCTGGACACAGCTGGGACCTTAGCTGTTACGGGCGAGTCTTATTCCTCGCTCAGCAGTCA	1864
Qy	1940	AGCAACTGAAGGTGGCGGTTTTGGCTGCAATGTCCTGTAACTCCCTGGATTACAATTGA	1999
Db	1865	AGCGCTCCAGCTGGCGCTTTCGCGCCCGCCCTCTGCACTCCCTGGAGTACAGCCTCC	1924
Qy	2000	GAGTTTACTGTGGGCAATACCCCTTGTGCAATTCAGGAAGTGGTTTCAATGAAAGGC	2059
Db	1925	GGGTCTACTGCTGGAGGACAGCCTGTAGCACTGAAGGAGTGTCTGGAGCTGGAGCGGA	1984
Qy	2060	ATCAAGGTGGACAGCTCCTCGAAGAACCAAAATGTGTCATTTCAAAAGGAATACCTTTA	2119
Db	1985	CTCTGGCGGATACCTTGGTGGAGAGCGGAAACCGCTAATGTTTCAAGGACAGTTACCACA	2044
Qy	2120	GTCTTCAGATTTCTGTCTCTTGATATTTCCCCCAATTCCTCTGAGAAATTAACCAATTCAC	2179
Db	2045	ACCTGGCGCTCTCCCTCCATGACCTCCCCCATGCCCATTTGGAGGAGCAGTCTGGCCA	2104
Qy	2180	CCTGCCAGGAAGTCCCTTTCTCCCGGTGTGTGCAGTAAACCGGACGCGCTGCATGTG	2239
Db	2105	AATACCAGGAGATCCCTTCTATCACATTTGGAGTGGCAGCCAGAAAGGCCCTCCACTGCA	2164
Qy	2240	CTTCTCTCGTGGAGGTTATACGCCCACTACGACCCAGCTGTCTCTGCAAAATCTGCATTC	2299
Db	2165	CTTTTCACCCTGGAGAGGACAGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGGTGC	2224
Qy	2300	GGCAGCTCAAAAGGCATGAACAGATCCTCCAAGTGCAGACATCAATCCTTAGAGAGTGAAC	2359
Db	2225	GGCAGTGAAGGGGAGGCCAGATATTCAGCTGCATACCACTCTGGCAGAGACACCTG	2284
Qy	2360	GAGAAACGAT--CACTTTCTTGGCAAGAGGACAGACATTTTCCCTGACACAGCTGGCC	2416
Db	2285	CTGGCTCCCTGGACACTCTGTGCTCTGCCCTGGCAGCACTGTACACACCACCGCTGGGAC	2344
Qy	2417	CCAAGCGCTTCAAAATTCCTTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCC	2476
Db	2345	CTTATGCTTCAAGATCCCACTGTCCATCGCCAGAGATATGCAACAGCCTAGATGCC	2404
Qy	2477	CCAAATGCCAAAGGCAAGACTGGCAGATGTTAGCACAGAAACAGAGATCAACAGGAATT	2536
Db	2405	CCAACTCACGGGGCAATGACTTGGCGGATGTTAGCACAGAAAGCTCTATATGGACCGGTACC	2464
Qy	2537	TATCTTATTTGCTTACACAAAGTAGCCCATCTGCTGTCTATTTTGAACTGTGGGAAGCTC	2596
Db	2465	TGAATTATTTTGGCAACAAAGCGAGCCCAACGGGTGTATCCTTGGAACTCTGGGAAGCTC	2524
Qy	2597	GTCAATCAGCATGATGGTGATCTTGACTCCCTGGCTGTGCTTGGAAAGATTTGGGAGGA	2656
Db	2525	TGCACGAGACGATGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGGAGATGGGCAAGA	2584
Qy	2657	CACACAGC	2664
Db	2585	GTGAGATG	2592

RESULT 10			
CQ842137			
LOCUS	CQ842137	2585 bp	DNA
DEFINITION	Sequence 784 from Patent EPI440981.		linear
ACCESSION	CQ842137		PAT 02-AUG-2004

[illegible]

QY 915 AGATAAATAAACCTTTCATGAATAATAAACCCCAAGCATTGAGATGCCAGGACATTGC 974  
 DB 478 AG-----GCATTGAGAAATGCCAGGACATTGC 504  
 QY 975 TTGTACTCGGGCTTGGGTGCTCGCTCGTGGCCGTTGAGTCCCTGGTCAATTTGGTGTAC 1034  
 DB 505 TTGTACTCGGGCTTGGGTGCTCGCTCGTGGCCGTTGAGTCCCTGGTCAATTTGGTGTAC 564  
 QY 1035 CTTTACAGACGGAGCCAGAGTGAATATGGCGTGGAGCGTCAATGACTCTTTCGCAATGAC 1094  
 DB 565 CTTTACAGACGGAGCCAGAGTGAATATGGCGTGGAGCGTCAATGACTCTTTCGCAATGAC 624  
 QY 1095 AGTGTGCTTCCAGACCTTCAACTTGAACACGCTCGTCAAGCCAGCAATATCATGAAC 1154  
 DB 625 AGTGTGCTTCCAGACCTTCAACTTGAACACGCTCGTCAAGCCAGCAATATCATGAAC 664  
 QY 1155 AATGATACAGAAATAATCCTTTGGTAACCTCCCTGCTCCCTGAATTTCTGCCATGAGCCAGA 1214  
 DB 665 -----GGTAACCTCCCTGCTCCCTGAATTTCTGCCATGAGCCAGA 702  
 QY 1215 TGTGACAGTGGAGCCGACATACAGCGGACCCATCTGTCTGAGGACCCCTCTGGACAGGA 1274  
 DB 703 TGTGACAGTGGAGCCGACATACAGCGGACCCATCTGTCTGAGGACCCCTCTGGACAGGA 762  
 QY 1275 GCTCATGACAGAGTCTCACTCTTTAAACCTTTGTCGGACATCAAAAGTGAAAGTCCAGAG 1334  
 DB 763 GCTCATGACAGAGTCTCACTCTTTAAACCTTTGTCGGACATCAAAAGTGAAAGTCCAGAG 822  
 QY 1335 CTGCTTCAATGCTTCCCTGGAGTGTCTGAGAGAGTGTAGTACACGCAAGCAATCATTC 1394  
 DB 823 CTGCTTCAATGCTTCCCTGGAGTGTCTGAGAGAGTGTAGTACACGCAAGCAATCATTC 882  
 QY 1395 CAGGACTTTTCCCTGAGGAAACCAACAGCTTTAGTACATGATCCAGCAAGCAATCATTC 1454  
 DB 883 CAGGACTTTTCCCTGAGGAAACCAACAGCTTTAGTACATGATCCAGCAAGCAATCATTC 942  
 QY 1455 GCCTCATACCAAAATCTGTCATCACTCCCAAGAGAGTGTAGTACACGCAAGCAATCATTC 1514  
 DB 943 GCCTCATACCAAAATCTGTCATCACTCCCAAGAGAGTGTAGTACATGATCCAGCAAGCAATCATTC 1002  
 QY 1515 CTTTGGCAATTTAGGGGGCGCTTAGTAAATGCAAAATACAGGGGTGAGCTTACT 1568  
 DB 1003 CTTTGGCAATTTAGGGGGCGCTTAGTAAATGCAAAATACAGGGGTGAGCTTACT 1056

RESULT 12  
 AX686445  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS  
 Edinger, S., Macdougall, J.R., Millet, I., Ellerman, K., Stone, D.J.,  
 Gerlach, V., Grosse, W.M., Alsbrook, J.P., Lepley, D.M., Rieger, D.,  
 Burgess, C.E., Casman, S.J., Spytek, K.A., Boldog, F.L., Li, L.,  
 Padigaru, M., Mishra, V., Patturajan, M., Shenoy, S., Rastelli, L.,  
 Tchernev, V.T., Vernet, C.A., Zerhusen, B.D., Malyankar, U.M., Guo, Y.,  
 Miller, C.E. and Gangolli, E.A.  
 Proteins and nucleic acids encoding same  
 Patent: WO 02057450-A 1 25-JUL-2002;  
 Curagen Corporation (US)  
 Location/Qualifiers  
 1..2860  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 TITLE  
 JOURNAL  
 FEATURES  
 source

Query Match 21.8%; Score 597; DB 6; Length 2860;  
 Best Local Similarity 54.3%; Pred. No. 14e-153;  
 Matches 1507; Conservative 0; Mismatches 1145; Indels 123; Gaps 10;  
 QY 13 GCGGCCACCGCAGGCGCGCGGAGGGCGCGCGCTGCTCCGCTGCTGGGGGTGTGC 72  
 DB 53 GGGAGCATGGGGGCCCGGAGCGGAGCTCGGGCGCGCTGCTGGCACTGCTGCTGCTGC 112  
 QY 73 TTCTGGGCGGAGGAGACCGCGCTGCCCGAGGAATGCAATGGCGAAGCCTTCCCGAA 132  
 DB 113 TGGGACCGGAGCTGAGCCAAAGCAGGCACTGATTTCTGGCAGGAGGTGCTTCCCTGACTCC 172  
 QY 133 TCCATCCCATCAGCTCTCTGGGACACTGCTCATTTTCATAGAGGAGCCAGATGATCTTAT 192  
 DB 173 TTCCGCTCAGCGCAGAGAGCGCTGCTCTTCTTCTGAGGAGCCACAGGACGCTAC 232  
 QY 193 ATTATCAAGAGCAACCTTATTTGCACTAGGTGCAAGAGGAGCCAGCATGAGATATTC 252  
 DB 233 ATTTGTAAGAACAGCTGTGGAGCTCGCTGCTGCGCGCTTCCCGCCACACAGATCTAC 292  
 QY 253 TTCAATTCGACGGGAGTGGTCCATCAGAACGAGCAGCTCTCTGAAAGAGACTCTGGAC 312  
 DB 293 TTCAATTCGACGGGAGTGGTCCAGAACGAGCAGCTCTCTGAAAGAGACTCTGGAT 352  
 QY 313 GAGAGCTCAGGTTTGAAGGTCCGGAAGTGTTCATCAATGTTTCTAGGCAACAGGTGGAG 372  
 DB 353 GAGGCCACCGCTCTCGGGTCCGCGAGGTGCAGATCGAGGTGCTCGCGCAGCAGGTGGAG 412  
 QY 373 GACTTTCATGGGCGCGAGGACTTATTTGGTGCAGTGTGTGGCGTGGAGCCACCTGGGTACC 432  
 DB 413 GAGCTCTTTGGGCTGGAGGATTTACTTGTGTCAGTGTGGCTGGAGCTCCGCGGGCAC 472  
 QY 433 TCCAGAGCAGGAGAGGCTCTCTGCGCATAGCTTATTTACGGAATACTTTGAAACAAGAC 492  
 DB 473 ACCAGAGTCTGCGGAGCTTACGCTCGCATCTGCTGCTGCGCAAGACTTTCATGAGTGT 532  
 QY 493 CCACAGGAGGAGGAGTTCCTTCCATTTGAAGGCAATGTTGTACTGCACTGCGCGCCACAGAG 552  
 DB 533 CCTTGGGCAAGGAGTGTCCCTGCAACATGAGTGTCTCTGCACTGCGCGCGCGCGGAG 592  
 QY 553 GAGTCTCTGCTGCGGAGTGGATGAGTGGTGAAGATGAGAGCCCATGACTCTGAACAA 612  
 DB 593 GGGGTGCTCTGCGGAGTGGATGAGTGGTGAAGATGAGAGTGTGATCGACCCACCCAG 652  
 QY 613 GACGAGAACATTGACACAGGCTGACCAATACCTGATCATCAGGAGGAGCAGGCTCTCG 672  
 DB 653 GACACCACTTCTGCTCACCATCGACCAACCTCATCATCGCCAGGCGCGCTGTGCG 712  
 QY 673 GACTCAGGAAATTACACCTGCAATGGCAGCCAAATGCTGCTGCTGCTGCTGCTGCTGCTG 732  
 DB 713 GACACTGCCAACTATACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 772  
 QY 733 GCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783  
 DB 773 GCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 832  
 QY 784 TCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843  
 DB 833 TCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 892  
 QY 844 AGAATTTGGGGGCAATTTCTGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871  
 DB 893 CTCACGAGGGGCTTCTTCTGCGAGGGCCAGGCAATTCAGAGACCGCTGTCACCAATC 952  
 QY 872 -----TAAGCCAGGAATCTGMAAATCTGCACAG----- 898  
 DB 953 TGCCCACTCGATGGGCGTGGAGGAGTGGAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1012  
 QY 899 -----ATGGTCTTTTGGCATCTTAGATAAAAAACCTCTTCTCATG 934  
 DB 1013 GCCCACTGGCGTAGCCGAGTGCATGGCGGCCCCACCCAGAACGAGGCGCTGCTGCTGCTGCTG 1072

```
QY 935 AATATAAACCACCAATTTGAGATGCCAGACGACATTGCTTTGTACTCGGGCTTGGGTG 994
Db 1073 AGCGGACGCTGCTCGCACTTAAGAACTGCACAGATGGGCTGTGCATGCAACTGAGAGGC 1132
QY 995 CTGCGCTCGTGGCGCTTGCAGTCTCTGTCTATTGGTGTACCCCTTTACAGACGAGCCAGA 1054
Db 1133 TCAGGGGATCGGGGCTGTATGCGGGGCTGTGGTGGCCATCTTCTGTGGTCTGTGGCAATC 1192
QY 1055 GTGACTATGCGGTGAGAGTCAITGACTCTTTCTGCAATGACAGTGGCTTCCAGA-CTTTC 1113
Db 1193 CTATGCGGCTGGGGGTGGTGGTGTACCGCGCAACTGCGCGTGAATTCGACATTCGACACAGACATC 1252
QY 1114 AACTTCAAAACAGTCCGTCAAGCCAGAAATATCATGGAATCAATGATACAGAAATATCC 1373
Db 1253 ACTGACTCATCTGCTGCCCTGACTGGTGGTTCACCCCGTCAACTTTAAGACGGCAAGG 1312
QY 1174 TTTGGTAACTCCCTGCTGCTGAATTTCTGCATGCGAGCCAGATCTGACAGTGAAG-CCGG 1230
Db 1313 CCCAGTAAACCGAGCTCTACACCCCTCTGTGCTCTGACCTGTGACGACGCGCGGC 1372
QY 1231 ACATACAGCGGACCCATCTGT-CTGAGGACCTCTGGAACAAGGAGTCTATGACAGAG 1287
Db 1373 ATCTACCGCGACCCGTGTATGCGCTGAGGACTCTCACCCGACAAATATCCCCATGACCAAC 1432
QY 1288 TCCTCACTCTTTAACCCCTTTGTGCGACATCAAGTGAAGTCCAGAGCTGTTCA----- 1342
Db 1433 TCTCCTCTGTCGACCCCTTACCGAGCTTTAAGTCAAGTCTACAGCTCCAGCAACG 1492
QY 1343 -TGGTTTCCCTGGAGTGTCTGAGAGAGTGAATACCAAGGCAAGATATTTCCAGACT 1401
Db 1493 GGCTCTGGGCGAGGCTGGAGATGGGCTGTACTGTGGGGTCTTTCGCGCTTGGCACA 1552
QY 1402 TTTTCCCATGGAACCAACACAGCTTTAGTACAAATGCAATCCCAAGAAATAAATGCCCTAC 1461
Db 1553 TACCCTAGCGATTTGGCGGGACACCCACTTCTCTGCACTGCGGCGGCGCAGCTCGGT 1612
QY 1462 ATCCAAATCTGTCACTCTCCCAACAGACAGACTGAGGACACTGTGTCTGTGGC 1521
Db 1613 TCCACGAGCTCTTGGGCGCTGCGCGGAGACCCAGGAGACGCTGACGCGCACCTTTGGC 1672
QY 1522 CATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTGAGCTTACTATACACACGCT 1581
Db 1673 TGCTGGTGGAGGCTCAGACATCCCGGACAGGGGTGAGCTTGTGTGCGCAATGGA 1732
QY 1582 GCCATCCAGAGAGAAATCTTGGGAGATTTATGTCCATCAACCAAGGTGAACCCAGC 1641
Db 1733 GCCATTTCCAGGCAAGTTCTAGAGATGTATCTACTCATCAACAGGCGAGAAAGTACC 1792
QY 1642 CTCAG---TCAGATGGCTCTGAGTGTCTCTGAGTCTCTGAAGTCACTGTGTCTCTCCA 1698
Db 1793 CTGCGGCTTTTCAAGAGGGACCCAGACAGTATTGAGCCCTCTCGGTGACCTGTGACCCACA 1852
QY 1699 GACATGATCTCACCACTCCCTTTGCAATTCACATCCCGACTGTGAGATGTCAGTTCT 1758
Db 1853 GGCTCTGTGTGCGCGCCCGTCACTCTCACAATGCCCCACTGTGCGGAAGTCAGTGCC 1912
QY 1759 GAGCATTTGGAATATCCATTTAAGAGAGAGGACACAGCAGGCGCAATGGGAGGAAGTATG 1818
Db 1913 CGTGACTGGATCTTTGAGCTCAAGACCCAGCGCCACAGGCGCACTGGGAGGAGTGGTG 1972
QY 1819 TCAGTGAAGATGAATC-----TACATCTGTGTACTGCTTTTGGACCCCTTTCGTGT 1872
Db 1973 ACCCTGGATGAGGAGACCTTGAACACACCCCTGTCTACGCCAGTGGAGCCGCGCTGT 2032
QY 1873 CATGTGCTCTGACAGCTTTGGGACCTATGCGTCTCACTGAGAGGACCAATCACAGACTGT 1932
Db 2033 CACATCTGTGTGACAGCTGGGACCTACTGTGTTCAGCGGCGAGTCTTATTCGCGTCA 2092
QY 1933 GCGGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCAATGTCTGTAACTCCCTGGATTC 1992
Db 2093 GCAGTCAAGCGGCTCCAGCTGGCGGTCTTCGCGCGCGCCCTCTGCACCTCTCCCTGGAGTAC 2152
QY 1993 AACTTGAGAGTTTACTGTGTGGACATATACCCCTTGTGCAATTCAGGAAGTGGTTTCAGAT 2052
```

```
Db 2153 AGCCTCCGGGTCTACTGCTTGGAGGACACCCCTGTAGCACTGAGGAGGTGCTGGAGCTG 2212
QY 2053 GAAAGGCATCAAGGTGGACAGCTCTCTGGAGAAACCAAAATTTGCTGCAATTTCAAGGGAAT 2112
Db 2213 GAGCGACTCTGGCGGATACTTTGGTGGAGGAGCCGAAACCGCTAATGTTTCAAGGACAGT 2272
QY 2113 ACCTTTAGTCTTCAGATTTTCTGCTTCTGATATTTCCCATTTCTCTGGAGAAATTAACCA 2172
Db 2273 TACCAACAAGCTGCGCTCTCCCTCCATGACCTCCCATGCCCCATTTGGAGGAGCAAGCTG 2332
QY 2173 TTCACCTGCTGCCAGGAAGTCCCGTTCTCCCGGTGTGGTGAGTAACCGGAGCCCTG 2232
Db 2333 CTGGCCAAATACAGAGATCCCTTCTATCAATTTGGAGTGGCAGCCAGAGGCCCTC 2392
QY 2233 CACTGTGCTTCTCCCTGGAGCGTTATACGCCCACTACACCCAGCTGTCTCTGCAAAATC 2292
Db 2393 CACTGCACCTTTCACCTGGAGAGGCAAGCTTGGCTTCCACAGAGCTCACCTGCAAGATC 2452
QY 2293 TGCAATTTGGGAGCTCAAGGCCATGAACAGATCTTCAAGTGCAGACATCAATCTTAGAG 2352
Db 2453 TGGCTGCGCAAGTGGAGGGGAGGCGCAGATATTCAGCTGCATACCACTCTGGGAGAG 2512
QY 2353 AGTGAACGAGAAACCAT---CACTTTTCGCAACAGAGACAGCACTTTCCCTGCACAG 2409
Db 2513 ACACCTGTGCTGCTTCCCTGGACACTCTGTCTGTGCCCCCTGGGAGCACTGTCAACCCAG 2572
QY 2410 ACTGGCCCCAAGCTTCAAAATTTCCCTACTCATCAGACAGCGGATTTGTGTACATTT 2469
Db 2573 CTGGGACCTTATGCCCTTCAAGATCCCACTGTCTCCAGAGAGATATGCAACAGCCTA 2632
QY 2470 GATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTAGCAGAGAAAACAGCATCAAC 2529
Db 2633 GATGCCCCCAACTCAACGGGGCAATGACTGGCGGATGTAGCAGAGAGCTCTCTATGGAC 2692
QY 2530 AGGAATTTATCTTATTTTCGTACACAAAGTAGCCCATCTGTCTCATTTTGAACCTCTGG 2589
Db 2693 CGGTACTGTAATTTACTTTGCCCAAGCGAGCCCAACGGGTGTGATCTCTGGACCTCTGG 2752
QY 2590 GAAGCTCGTCATCAGCATGATGTTGATCTTGAATCCCTTGGCCTGTGCTTGAAGAGATT 2649
Db 2753 GAAGCTCTGCGCAGGACGATGGGACCTCAACAGCTTGGCGAGTGGCTTGGAGGAGATG 2812
QY 2650 GGGAGGACACACAGC 2664
Db 2813 GGCAAGAGTGAGATG 2827
```

## RESULT 13

```
AX686447
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
```

AX686447 2860 bp DNA linear PAT 29-MAR-2003  
Sequence 3 from Patent WO02057450.  
AX686447  
AX686447.1 GI:29372154  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Edinger, S., Macdougall, J.R., Millet, I., Ellerman, K., Stone, D.J.,  
Gerlach, V., Grosse, W.M., Alsbrook, J.P., Lepley, D.M., Rieger, D.,  
Burgess, C.E., Casman, S.J., Spytek, K.A., Boldog, F.L., Li, L.,  
Padigara, M., Mishra, V., Patturajan, M., Shenoy, S., Rastelli, L.,  
Tchernev, V.T., Vernet, C.A., Zerhusen, B.D., Malyankar, U.M., Guo, Y.,  
Miller, C.E. and Gangolli, E.A.  
Proteins and nucleic acids encoding same  
Patent: WO 02057450-A 3 25-JUL-2002;  
Curagen Corporation (US)  
Location/Qualifiers  
1..2860  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"

ORIGIN		/db_xref="taxon:9606"	
Query Match		21.8%; Score 592.2; DB 6; Length 2860;	
Best Local Similarity		54.2%; Pred. No. 3.1e-152;	
Matches 1504; Conservative		0; Mismatches 1148; Indels 123; Gaps 10;	
QY	13	GCAGCCACCGCAGCGCGCGGAGGGGCGCGCGCTGCTCCCGTGGCTGGGGCTGTGC	72
DB	53	GGGAAATGAGGGGCCCGAGCGAGCTCGGGGCGCGCTGCTGCTGCACTGCTGCTCTGC	112
QY	73	TTCTGGCGCGCAGGAGCCGCGGCTGCTCCGAGGAATGACAAATGGCGAAGCCCTTCCCGAA	132
DB	113	TGGGACCCGAGGCTGAGCCAAAGCAGCACTGATTCTTGGCAGCGAGGTGCTCCCTGACTCC	172
QY	133	TCATCCCATCAGCTCTGCGGACATGCTCTCATTTTCATAGAGGAGCAGATGATGTTAT	192
DB	173	TTCCCGTCAGCGCAGCAGAGCGCGCTGCTTCTCTGCGAGGACCAAGGACGCGCTAC	232
QY	193	ATTATCAAGAGCAACCTATTGCACTCAGGTGCAAGCGAGGCGAGCCATGCAATATTC	252
DB	233	ATTGTGAAGAACAGGCTGTGAGGCTTGGTGGCGGCTTCCCGCCACACAGATCTAC	292
QY	253	TTCAATGCAACCGCGAGTGGTCCATCAGAACGAGCAGCTCTCTGAAGAGACTTGGAC	312
DB	293	TTCAAGTGCAACCGCGAGTGGTCCAGCAAGCAGCACGCTCAACAGGAAGCGCTGGAT	352
QY	313	GAGAGCTCAGGTTGAAGTCCGGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAG	372
DB	353	GAGGCCACCGCGCTGCGGGTGCGGAGGTGCAGATCGAGGTGTCGCGGAGCAGGTGGAG	412
QY	373	GACTTCCATGGGCGCGAGGACTATTGGTCCAGTGTGTGGCGTGGAGCCACCTGGGTACC	432
DB	413	GAGCTCTTTGGGCTGGAGGATTAAGTGGTCCAGTGTGGTGGCTGGAGCTCGCGAGCAC	472
QY	433	TCCAAAGCAGGAAGGCTCTGTGCGCATAGCTTATTTAGCGAAAACTTTGAAACAGAC	492
DB	473	ACCAAGAGTCCCGAGCTACGTCCGCGCATCGCTTACCTGCGCAAGAACTTCGATCAGGAG	532
QY	493	CCACAGGAGGAGGATTTCCCATTTGAGGCGATGATTTGCTGCTGCGCCCGCCACAGAG	552
DB	533	CCCTTGGGCAAGAGGTGGCCCTTGACCATGAGGTCTCTGCGAGTCCGCCCGCGCGAG	592
QY	553	GGAGTCCCTGCTGCGAGGTGGAATGGCTGAAATGAAGAGCCATTTGACTCTGAACAA	612
DB	593	GGGTGCTCTGTGCGGAGTGGATGGCTCAAGAAATGAGATGCTATCGACCCACCCAG	652
QY	613	GACGAGAACATTGACACAGGGCTGACCATTAACCTGATCATCAGGCGAGGACCGCTCTCG	672
DB	653	GACACCAACTTCTGCTCACCATCGACCAACACCTCATCTCCGCGAGGCCCGCTGTGCG	712
QY	673	GACTCAGGAATTAACCTCATGCGGAGCCAAACATCGTGGCTAAGAGGAGAGCCTGTGCG	732
DB	713	GACACTGCCAACTATATCTGCTGGCCCAAGAACATCGTGGCCAAACGCCGAGGACCACT	772
QY	733	GCCACTGTTGTGCTCTACGTGGATGG-----GAGCTGGGAAGTGTGGAGCGAATGG	783
DB	773	GCCACCGCTCATCTGCTACGTGAAATGGCGGCTGGTCCAGTGGGCGAGGTGCTCACCTGC	832
QY	784	TCGCTCTCAGTCCAGAGTGTGAACATTTGGGATCCGGAGTGGCAGCAGCACCCCGG	843
DB	833	TCCAACCGCTGTGGCCGAGGCTGGCAGAGCGCACCCGAGCTGCAACACCCCGCTCCA	892
QY	844	AGAAATGGGGCAAAATTTCTGTAAGGTC-----	871
DB	893	CTCAACGAGGGGCTTCTGGAGGGCCAGGCATTCCAGAAAGCCGCTGCACCAACATC	952
QY	872	-----TAAGCCAGGAATCTGAAACTGGACAG-----	898
DB	953	TGCCCACTCGATGGGGCGTGGAGCGAGTGGAGCAAGTGGTCAGCGCTGCAGCACTGAGTGT	1012
QY	899	-----ATGCTCTTTGCATCTTAGATAAAAAACCTCTTCATG	934
DB	1013	GCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCGCCACCCAGAAACGAGGAGCGGTGACTGC	1072
QY	935	AAATAAAACCCCAAGAGCATTCAGAAATGCCAGCGACATTTGTTGTTACTCGGGCTTGGGTG	994
DB	1073	AGCGGAGCGTGTCTGCACTTAAGAACTGACAGATGGGCTGTGATCACTCAACTGGAGGCC	1132
QY	995	CTGCGCTGCTGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1054
DB	1133	TCAGGGGATGCGGCGCTGATGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1192
QY	1055	GTGACTATGGCTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1113
DB	1193	CTCATGGGCGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1252
QY	1114	AACTTCAAAAACAGTCCGCTCAAGCCAAAGAAATATCATGGAATAATGATCAAGAAAAATCC	1173
DB	1253	ACTGACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1312
QY	1174	TTTGGTAACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1230
DB	1313	CCAGTAAACCGCGAGCTCTACACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1372
QY	1231	ACATACAGGGGACCCATCTGT---CTGCGAGGACCTCTGCGACAGGAGCTCATGACAGAG	1287
DB	1373	ATCTACCGCGGACCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1432
QY	1288	TCCTCACTCTTTAAACCTTTGTCGACATCAAAAGTGAAGTCCAGAGCTGCTGCTCA-----	1342
DB	1433	TCCTCTCTGCTGACCCCTTACCCAGCCTTAAAGGTCAAGGTCTACAGCTCCAGCACCAG	1492
QY	1343	-TGGTTTCCCTGGAGTGTCTGAGAGAGCTGAGTACAGGAGGAGGAGGAGGAGGAGGAGG	1401
DB	1493	GGCTCTGCGGCCAGGCGCTGCGAGATGGGGCTGACCTGCTGGGGGTCTTGCGCGCTGGCACA	1552
QY	1402	TTTTTCCCATGGAACAAACACAGCTTTAGTACAAATGCAATCCAGAAATAAATGCGCTAC	1461
DB	1553	TACCTTAGCGATTTGCGCGGAGACCCACTTCTCTGCACTTCTGCGAGCGCCAGCTCGGT	1612
QY	1462	ATCCAAATCTGCTCATCTCCCAAGGACAGAACTGAGGACAACTGCTGCTTGTGGC	1521
DB	1613	TCCAGCAGCTCTTGGGCGCTGCGCGAGACCCAGGAGCAGCGTCAAGCGGACCTTTGCG	1672
QY	1522	CAITTAGGGGGCGCTTAGTAATGCCAATACAGGGGTGAGCTTACTATACACACAGCT	1581
DB	1673	TGCTGCTGGTGGAGGCTCAGCATCCCGGCAAGGGGTGAGCTTCTGCTGCTGCTGCTGCTG	1732
QY	1582	GCCATCCAGAGGAGAAATCTTTGGGAGATTATATGTCATCAACCAAGGAGGAGGAGGAG	1641
DB	1733	GCCATTTCCAGGCGCAAGTTCTACGAGATGATCTACTCATCAACAAAGGAGGAGGAGTAC	1792
QY	1642	CTCCAG---TCAGATGGCTCTGAGGTGCTCTGAGTCTCTGAGTCTGAGTCTGAGTCTGAG	1698
DB	1793	CTGCGCTTTCAAGAGGAGCCAGACAGATTATGAGGCCCTCGGTGACCTTGGGACCCACA	1852
QY	1699	GACATGATCGTCAACCTCTTTCATGATGACCATCCGCACTGTCAGATGTCAGTGTCT	1758
DB	1853	GGCTCTGCTGCTGCGCGCCCGCTCATCTTCAACATGCCCTGCTGCTGCTGCTGCTGCTG	1912
QY	1759	GAGCATTTGGAATATCCATTTTAAAGAGAGGACACAGAGGCGCAAAATGGGAGGAGGAGT	1818
DB	1913	CGTACTGATCTTTTCAGCTCAAGACCCAGGCCACCAAGGCGCACTGGGAGGAGGAGTGTG	1972
QY	1819	TCAGTGGAAAGATGAATC-----TACATCTGTTACTGCTTTTGGACCCCTTGGGTGT	1872
DB	1973	ACCTGGATGAGGAGACCTCGAAACACACCTGCTACTGCGAGCTGGAGCCGAGGCTGT	2032
QY	1873	CATGCTCTCTGAGAGCTTTGGGACCTATGCGCTCATCTGGAGAGGCAATCAACAGACTGT	1932
DB	2033	CACATCTGCTGAGCAGCTGGGACCTTACGTTTCAAGGCGAGTCTTATTTCCCGCTCA	2092
QY	1933	GCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGATGCTGCTGTAATCTGCTGCTGCTG	1992
DB	2093	GCACTCAAGCGGCTCCAGCTGCGCTTTCGCGCCCGCTCTGCACTCTCTCTGCTGCTG	2152



Qy	1993	AAC	TGAGAGTTT	ACTG	TGTGGACA	ATAC	CCCTTGTG	GCATTT	CAGGAAGTGT	TTTCAGAT	2052					
Db	2153	AGC	CTCGGGT	CTACTG	CTGTGGAG	CACG	CCCTGTAG	CAC	TGAAGAGG	TGCTGGAG	CTG 2212					
Qy	2053	GAA	AGGCAT	CAAGT	TGGACAG	CTCT	TGGAAG	CAAAAT	TGTCG	CATTTCA	AAAGGAAT 2112					
Db	2213	GAG	CGA	CTG	GGCGG	ATCT	TGTGGAG	GCGGA	ACG	CTAATG	TTTCAGGACGT 2272					
Qy	2113	AC	TTTAGT	CTTTAG	ATTTCT	GTGAT	ATAT	CCCCA	TTCTCT	CTGGAGA	ATTAACCA 2172					
Db	2273	TAC	CACA	ACCT	TCGC	CTCT	CCCTCAT	GAC	CTCC	CCCATG	CCCATTTGGAGGAGCAAGCTG 2332					
Qy	2173	TT	CACTG	CTG	CCAGGA	AGTCC	CGTCT	CCGCG	CTGTG	TCAGT	ACCGGACGCCCCCTG 2232					
Db	2333	CT	GGCA	ATATAC	AGAG	ATCCCC	CTTTAT	CAC	ATTTGG	ATGGC	ACCAAGGCCCTC 2392					
Qy	2233	CAC	TGTG	CTTCT	CCCTGG	AGCG	TTATAC	GGCCCA	CTACCA	CCCA	CGTGTCTCTGC	CAAAATC 2292				
Db	2393	CAC	TGCA	CTTT	CAC	CTTGG	AGGCA	CAG	CTTGG	CCCTCC	CAGAGCTCA	CTGCAAGATC 2452				
Qy	2293	TGC	ATTT	CGG	CAGCT	CA	AGGCC	ATGA	CAG	ATCT	CCAAGTGC	GAGACATCAATCCTTAG 2352				
Db	2453	TGC	TGTGG	CGGA	GTGG	AAAGGG	GCGG	CCAG	ATAT	TCCAG	CTGTGC	ATACCATCTCTGGCAGAG 2512				
Qy	2353	AGT	GAA	CGAG	AAAA	CCAT	---	CAC	TTTTCT	TG	CAAGAGG	ACACGACTTTTCCCTG	GCACAG 2409			
Db	2513	AC	ACTG	TG	TGG	CTCC	CTGG	ACAC	CTCTG	CTCTG	CCCTGG	CACACTGTGTCA	CCACCAC 2572			
Qy	2410	ACT	GGCCCC	AAAG	CTTCA	AAAT	TTCC	CTAT	CTC	ATC	AGAC	AGCGGATTTGTG	CTACATTT 2469			
Db	2573	CT	GGGAC	CTTAT	TG	CTTT	CA	AGAT	CCCA	CTGT	CCATCC	GCCAGAGA	TATGCA	CAGCCTA 2632		
Qy	2470	GAT	AC	CCCC	CAATG	CA	AGGCA	AGCA	CTGG	CAG	ATGTTAG	CACAG	AAAA	CAGCAT	CAAC 2529	
Db	2633	GAT	CCCC	CCCA	CTCA	CG	GGGCA	ATGA	CTGG	CGG	ATGTTAG	CACA	CAGA	AGCTCT	CTATGGAC 2692	
Qy	2530	AG	GAAT	TTATCT	TAT	TTG	CGT	PACA	CA	AA	GTAG	CCCAT	CTCTG	TGTCAT	TTTGA	ACCTGTGG 2589
Db	2693	CG	GTAC	CTG	ATTTACT	TTT	GG	CACCA	AG	CGAG	CCCA	CGG	GTGTG	ATCTCT	CTGG	ACCTCTGG 2752
Qy	2590	GA	AG	CTG	TCAT	CAG	CAT	GAT	GTG	TG						

RESULT 14  
 CQ850929  
 LOCUS 3933 bp DNA linear PAT 23-AUG-2004  
 DEFINITION Sequence 1398 from Patent EP1447413.  
 ACCESSION CQ850929  
 VERSION CQ850929.1 GI:51509141  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 Isogai, T., Yamamoto, J., Nishikawa, T., Isono, Y., Sugiyama, T.,  
 Oeuki, T., Wakamatsu, A., Ishii, S., Nagai, K. and Irie, R.,  
 Full-length human cDNA  
 Patent: EP 1447413-A 1398 18-AUG-2004;  
 Research Association for Biotechnology (JP)  
 Location/Qualifiers  
 1..3933  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 FEATURES  
 source

Query Match	21.6%	Score 590.2	DB 6	Length 3933
Best Local Similarity	54.7%	Pred. No. 1.1e-151		
Matches 1562	Conservative 0	Mismatches 1048	Indels 243	Gaps 10
Qy	13	CGCGCCACCGCAGCGCGCGCGGAGGCGGCGCGCTGGCTCCCGTGGCTCGGGCTGTGC	72	
Db	446	GGGAGCATGTGGGGCCCGGAGCGAGCTCGGGGCGCGCTGCTGTGGCACTGCTGCTCTGC	505	
Qy	73	TTCTGGCGCGCAGGACCGCGGTGCCCGGAGGAATGACAAATGCGGAAGCCCTTCCCGAA	132	
Db	506	TGGGACCGGAGGTGAGCCAAAGCAGGACTGATTTCTGGCAGCAGGTGCTCCCTGACTCC	565	
Qy	133	TCCATCCCATCAGCTCCTCGGACACTGCCCTCATTTTCATAGAGGACGAGATGATCTTAT	192	
Db	566	TTCCGCTCAGCGCAGCAGACCGCTGCCCTACTTCTCTGCAAGGACCACAGGACGCCATC	625	
Qy	193	ATTATCAAGAGCAACCTATTTCACCTCAGGTGCAAGCAGGCGCAGCCATGCAATATTC	252	
Db	626	ATTGTGAAGAACAGCCTGTGGAGCTCCGCTGCGCGCTTCCCGCCACACAGATCTAC	685	
Qy	253	TTCAATATGCAACGCGAGTGGTCCATCAGAACGACGACGCTCTCTGAAGAGACTCTGGAC	312	
Db	686	TTCAAGTCAACGCGAGTGGTTCAGCCAGAACGACCACTCAACAGGAAGCCTGGAT	745	
Qy	313	GAGAGCTCAGGTTTGAAGGTCCGGAAGTTCATCAATTTTACTAGGCAACAGGTGGAG	372	
Db	746	GAGGCCACCGCCTCGGGTGCAGAGTGCAGATCGAGGTTCGCGGCAGCAGGTGGAG	805	
Qy	373	GACTTCATGGGCCGAGGACTATTGGTGCAGTGTGGCGTGGAGCCACCTTGGGTACC	432	
Db	806	GAGCTCTTTGGGCTGGAGGATTAAGTGTGCAGTGGCTGGAGCTCCGCGGCGCAC	865	
Qy	433	TCCAAGACAGGAAGGCCTCTGTGCGCATAGCCTATTTCGGAATAACTTTGAACAAGAC	492	
Db	866	ACCAAGAGTCGCGAGCCTACGTCCGATCGCCTACCTGCGCAAGAACTTCGATCAGAG	925	
Qy	493	CCACAGGAAGGAAGTTCCCATTTGAAGGCATGATTTGTAATGCACTGCCGCCACACAGAG	552	
Db	926	CCTCTGGCAAGAGGTGCCCTTGACCATGAGTTCTCTGCACTGCCGCCCGCGGAG	985	
Qy	553	GGAGTCCCTGCTGCGAGGTGGAAATGGCTGAATAATGAAGAGCCCATTTGATCTGAACAA	612	
Db	986	GGGCTGCTGTGGCCGAGTGGAAATGGCTCAAGAATGAGGATGTCATCGACCCACCCAG	1045	
Qy	613	GACGAGACATTGACACCAGGCTGACCAATACTGATCATCAGGACGAGCAGGCTCTCG	672	
Db	1046	GACACCAACTTCTGCTCACCATCGACCAACAACTCATCATCGCAGGCGCCGCTGTG	1105	
Qy	673	GACTCAGGAATATACCTCATGGACGACCAACATCGTGGCTAAGAGGAAGCCTGTGCG	732	
Db	1106	GAACTGCCAACTTATACCTGCTGGCCAGAAACATGTTGGCCAAAAGCGCGAGCACT	1165	
Qy	733	GCCACTGTTGTGTTACTAGTGGATGGAGCTGGGA	767	
Db	1166	GCCACGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGACAGTGGTCACTCC	1225	
Qy	768	-----	767	
Db	1226	TCCAACGCTGTGCGGAGCTGGCAGAAAGCGACCCGGACCTGCAACCAACCCCGTCCA	1285	
Qy	768	-----	767	
Db	1286	CTCAACGGAGGGCCTTCTCGAGGGCCAGGCATTCAGAAAGCCGCTGCACCACTC	1345	
Qy	768	-----AGTGTGGAGCGAAATGGTCCGTCTGCACTGCAGTAGTGT	804	
Db	1346	TGCCAGTCGATGGGGCTGGACGGAGTGGCAAGTGGTTCAGCTGCAGCACTGAGTGT	1405	
Qy	805	GAACTTTGGGATTCGGGAGTGACAGCAACACCCCGAGAAATGGGGGCAAAATTTCTGT	864	
Db	1406	GCCACTGGGCTAGCCGAGTGCATGGCGCCGCCACCCAGAACGGAGCGCTGACTGC	1465	

## ORIGIN



JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 3933)  
Isogai,T. and Yamamoto,J.  
Direct Submission  
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7  
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan  
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction: Helix Research Institute (HRI) (supported by Japan  
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
HRI, and Biotechnology Center, National Institute of Technology and  
Evaluation; clone selection for full insert sequencing: HRI and  
RAB; annotation: Reverse Proteomics Research Institute, HRI and  
RAB.

FEATURES  
Source

Location/Qualifiers  
1..3933  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="TEST14022158"  
/tissue\_type="testis"  
/clone\_lib="TEST14"  
/note="cloning vector: pME18SFL3"

## ORIGIN

Query Match 21.6%; Score 590.2; DB 9; Length 3933;  
Best Local Similarity 54.7%; Pred. No. 1.1e-151;  
Matches 1562; Conservative 0; Mismatches 1048; Indels 243; Gaps 10;  
  
QY 13 GGGGCCACCGAGCGCGCGGAGGGCGCGCGTGGCTCCCGTGGGTGGGGGTGTGC 72  
DB 446 GGGAGCATGGGGCCCGAGCGAGCTCGGGGGCGCTGTGTGCACTGTCTCTGC 505  
QY 73 TTCTGGCGCGAGGACCGCGCTGCCGAGGAACCTGCAATGGCGAAGCCCTCCGAA 132  
DB 506 TGGGACCCGAGGCTGAGCAAGCAGGCACTGATTCCTGGCAGCGAGTGTCTCCCTGACTCC 565  
QY 133 TCATCCCATCAGCTCTCTGGGACATCGCTCTCAATTCATAGAGGAGCGAGATGCTTAT 192  
DB 566 TTCCCGTACGCGCAGCAGCGCGTCCCTACTTCTTCGAGGAGCCACAGGACGCTAC 625  
QY 193 ATTATCAAGAGCAACCTTATGTCATCAGGTGCAAGCGAGGCGCAGCCATGCAATATTC 252  
DB 626 ATTGTGAAGAAACAAGCTGTGAGCTCCGTGCGCGCTTCCCGCCACACAGATCTAC 685  
QY 253 TTCAATGCAACGGCGAGTGGTCCATCAGACGACGCTCTCTGAAGAGCTCTGGAC 312  
DB 686 TTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACGCTCACACAGGAAGCCCTGGAT 745  
QY 313 GAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTTACTAGGCAACAGGTGGAG 372  
DB 746 GAGGCCACCGGCTCGGGTGGCGAGGTGCAGTCGAGGTGTGCGGCGAGAGTGGAG 805  
QY 373 GACTTCATGGGCCCGAGGACTATTGGTCCAGTGTGTGGCGTGGAGCCACCTGGGTACC 432  
DB 806 GAGCTCTTTGGGCTGGAGGATTACTGTGTCAGTGGTGGCTGGAGCTCCGCGGCAAC 865  
QY 433 TCCAGAGCAGGAGGAGGCTCTGTGCCATAGCTATTTACGGAAACCTTTGACAGAC 492  
DB 866 ACCAAGAGTGGCGAGGCTACGTCCGCATCGCTTACCTCGCAAGAACTTCGATCAGGAG 925  
QY 493 CCAGAGGAGGAGGAGTTCCTCAATTGAAGGCATGATTGTACTGCACTCGCGCCCAACAGAG 552  
DB 926 CCTCTGGCAGAGGAGTGGCCCTGGACATGAGGTTCCTCTGAGTGGCGCGCGGAG 985  
QY 553 GAGTCCCTGTGCGGAGGTGGAAATGGCTGAAATGAAAGAGCCCATTTGACTCTGAACAA 612  
DB 986 GGGGTGCTGTGGCGGAGGTGGAAATGGCTCAAGAAATGAGGATGTCATCGACCCCAACCC 1045  
QY 613 GACGAGCAATTGACACCGAGGCTGACCATTAACCTCATCATCAGGAGGCAAGGCTCTCG 672

DB 1046 GACACCAACTTCTGTCTACCATCGACCAACACCTCATCATCGCCAGGCGCCCTGTGC 1105  
QY 673 GACTCAGGAAATATACCTGTCATGGCAGCAACATCGTGGCTAAGAGGAGAACCTGTGTCG 732  
DB 1106 GACACTGCCAACTATACCTGCGTGGCCAAAGAACATCGTGGCCAAACGCGGAGCACCCT 1165  
QY 733 GCCACTGTTGTGTCTACCTGATGGAGAGCTGGGA----- 767  
DB 1166 GCCACCGTCATCGTCTACCTGATGGCGCTGGTCCAGCTGGGCGAGTGGTCAACCTGTC 1225  
QY 768 ----- 767  
DB 1226 TCCNACCGCTGTGGCGAGGCTGGCAGAGCGCACCGGACCTGACCAACCCGGCTCCA 1285  
QY 768 ----- 767  
DB 1286 CTCNACGGAGGGCGCTTCTCGAGGGCCAGGCAATTCAGAAAGACCGCTGCACCACCATC 1345  
QY 768 -----AGTGTGGAGGAATGTCCTGCTTGCAGTCCAGAGTGT 804  
DB 1346 TGGCCAGTCGATGGGGCGTGGAGCGGAGTGGAGCAAGTGTGCTGACCTGCGAGCATGAGTGT 1405  
QY 805 GAACATTTTCGGATCCGGAGTGCACAGCACACCCCGAGAAATGGGGGCAAAATTCCTGT 864  
DB 1406 GCCACTGCGTAGCGCGAGTGCATGGCGCCCGCCACCCAGNACCGAGGCCCTGACTGC 1465  
QY 865 GAAGTCTAAGCCAGGAATCTGAAAATCTGACAGATGGTCTTTGCAATCTAGATAAAAA 924  
DB 1466 AGCGGAGCGCTGCTGACTCTAAGAACTGCACAGATGGGCTGTGATGCAATAAGAAA 1525  
QY 925 CCTCTTCATGAATAAACCACCAAGCATTGAGATGCCAGGACATTTGTTTGTACTCG 984  
DB 1526 ACTTAAGCGACCCCAACAGCACCTGCTGAGGCGCTCAGGGGATCGCGCTGTATGCG 1585  
QY 985 GCTTGGGTGCTGCGTGTGCGCTTGCAG-----TCTGTGTCATTGTGTGCACCTT 1038  
DB 1586 GGGCTGCTGTGGCCATCTTGTGTGTGGCAATCTCATGGCGTGGGGTGGTGTG 1645  
QY 1039 TACAGCGGAGCCAGAGTGAATATGGCGTGGAGCTCATTTGAC-----TCTTGTGATGACA 1095  
DB 1646 TACCGCGCACTGCGCTGACTTCGACACAGACATCACTGACTCATCTGTGCCCTGACT 1705  
QY 1096 GGTGGCTTCAGACCTTCAACTTCAAAACAGTCCCTCAAGCCAGCAAGATATCATGGAACTA 1155  
DB 1706 GGTGGTTTCCACCGCTCAACTTTAAGACGGCAAGGC----- 1742  
QY 1156 ATGATACAGAAAAATCTTGTGTAATCTCTGCTCTGAAATTCGCAATGACGCGAGAT 1215  
DB 1743 -----CCAGCAACCCGAGCTCTTACACCCCTCTGTGCTCTCTGAC 1783  
QY 1216 CTGACAGTGAAG-----CCGGAACATACAGCGGACCCATCTGT---CTGAGGAGCCCTCTGGAC 1269  
DB 1784 CTGACAGCCAGCGCGGCATCTACCGCGACCGCTGTATGCGCTGCGAGCTCCACCGAC 1843  
QY 1270 AAGGAGCTATGACAGAGTCTCATCTTTTAACCTTTGTGCGACATCAAGTGAAGTC 1329  
DB 1844 AAAATCCCATGACCAACTCTCTCTGTGCGACCCCTTACCCAGCCCTTAAGGTCAAGGTC 1903  
QY 1330 CAGAGCTGCTTCA-----TGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAACGCGC 1383  
DB 1904 TACAGCTCAGCACCAAGGGGCTCTGGGCCAGGCTGGCAGACGGGGCTGACCTGTCTGGGG 1963  
QY 1384 AAGAAATCATTCAGGAGCTTTTCCCAATGGAAAACAACACAGAGCTTTTATGTAATGCAATCCC 1443  
DB 1964 GTCTTGGCGCTGGCACATACCTAGCGATTTTCGCCCGGAGACACCCACTTCTCTGCACCTG 2023  
QY 1444 AGAAATAAATGCGCTTACATCCAAATCTGTCTCATCTCTCCCAACAGGACAGAGCTGAGG 1503  
DB 2024 CGCAGCGCAGGCTCGGTTCCAGCAGCTCTTGGGCTTGGCCCGAGACCCAGGAGGAGCAGC 2083  
QY 1504 ACACTGTGTCTTTTGGCCATTTAGGGGGCGCTTAGTAATGCAAAATACAGGGGTGAGC 1563  
DB 2084 GTCAGCGGCACCTTTTGGCTGCTTGGTGGAGGCTCAGCATTCCTCGGCAAGGGGTGAGC 2143

Qy 2632 TGTGCTTGAAGAGATTGGAGGACACACACG 2664  
 Db 3224 AGTGCCTTGGAGGAGATGGGCAAGAGTGAGATG 3256  
 Search completed: April 1, 2005, 05:14:27  
 Job time : 11613 secs

1564 TTACTCATACACACAGGTGCCATCCAGAGGAGAAATCTTGGAGATTATATGTCCATC 1623  
 2144 TTGCTGGTCCCAATGGAGCCATCCCAAGGCAAGTTCTACGAGATGATCTACTCATC 2203  
 1624 AACCAAGGTGAACCCAGCCTCCAG---TCAGATGGCTCTGAGGTGCTCCTGAGTCCGAA 1680  
 2204 AACAGGCAAGATGATCCCTCCGCTTTCAGAGGACCCACACAGTATTGAGCCCTCG 2263  
 1681 GTCACTGTGGTCTCCAGACATGATCGTCAACATCTCCCTTTGCAATTGACCATCCGGCAC 1740  
 2264 GTGACCTGTGGACCCACACAGCCTCCTGTGTGCGCCCGCTCATCCTCACCATTGCCAC 2323  
 1741 TGTGCAGATGTCAGTTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACAGAGGC 1800  
 2324 TGTGCCGAAGTCAGTCCCGTACTGATCTTTTCACTCAAGACCCAGGCCACAGGC 2383  
 1801 AAATGGGAGAGTGTAGTGTGAGTGAAGATGAATC-----TACATCTCTGTTTACTGCTT 1854  
 2384 CACTGGGAGAGTGTGTGACCTCGATGAGGAGACCTTGAACACACCCCTGCTACTGCCAG 2443  
 1855 TTGGAACCTTTGCGTGTGATGCTCTGAGACAGCTTTGGGACCTATGGGCTCACTGGA 1914  
 2444 CTGGAGCCAGGCGCTGTACATCTCTGCTGGACAGCTGGGACCTTACGTGTTCAAGGC 2503  
 1915 GAGCCATCACACAGCTGTGCGTGAAGCACTGAAGTGGCGTCTTTTGGCTGCTGCTCC 1974  
 2504 GAGTCTATTTCGCTCAGAGTCAAGCGCTTCCAGCTGGCGTCTTCCGCGCCGCTC 2563  
 1975 TGTAACTCCCTGGAATTACAACTTTGAGATTTTACTGTGTGACAAATACCCCTTGTGCAATT 2034  
 2564 TGCACTCTCTGGATACAGCTCCGCTTCTACTGCTGGAGGACACGCTGTAGCACTG 2623  
 2035 CAGGAAGTGTCTCAGATGAAGGCATCAAGTGGACAGCTCCTGGAAGAACCAATTTG 2094  
 2624 AAGGAGGTGTGGAGTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAACCG 2683  
 2095 CTGCATTTCAAGGGAATACCTTTAGTCTTCAGATTTCTGCTCTTGATATTTCCCCCATTC 2154  
 2684 CTATGTTCAAGNACAGTTACCAACACCTCGGCTCTCCCTCCATGACCTCCCCCATGCC 2743  
 2155 CTCTGGAGAAATTAACCAATTCATGCGCTGCGAGAGTCCCGTTCTCCCGGTGTGGTGC 2214  
 2744 CATTTGGAGGAGCAAGCTGTCTGGCAATATACAGGAGATCCCTTCTATCATATTGGAGT 2803  
 2215 AGTAAACCGGAGCCCTGCACTGTGCTCTCTCTGGAGGTTATACGCCACTACCAAC 2274  
 2804 GGCAGCCAGAGGCCCTCCACTGCTTCCCTTGGAGGAGGACAGCTTGGGCTCCACA 2863  
 2275 CAGCTGTCTGCAAAATCTGCATTTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTG 2334  
 2864 GAGCTCACCTGCAAGATCTGGTGGCGCAAGTGGAGGGGAGGCCAGATATTTCCAGCTG 2923  
 2335 CAGACATCAATCTTAGAGAGTGAAGAGAACCAT---CACTTCTTTCGACACAGAGGAC 2391  
 2924 CATACCACTCTGGCAGAGACCTGTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCTTGGC 2983  
 2392 AGCACTTTCCCTGCACAGACTGGGCCCAAGCCCTTCAAAATTCCTACTCTCATCAGACAG 2451  
 2984 AGCACTGTACCAACCCAGCTGGGACCTTATGCTTCAAGATCCCACTGTCCATCCGCGCAG 3043  
 2452 CGGATTTGTGTACATTTGATACCCCAATGCCCCAAGCAAGGAGCTGGCAGATGTTAGCA 2511  
 3044 AAGATATGCAACAGCCTAGATGCCCCCAACTCACGGGCAATGACTGGCGGATGTTAGCA 3103  
 2512 CAGAAAACAGCATCAACAGGAATTTATCTTTTCTGCTACACAAAGTACGCCATCTGCT 2571  
 3104 CAGAACTCTCTATGGACCGGTACTGAAATTTACTTTGCCCACAAAGCGAGGCCCGCGGT 3163  
 2572 GTCATTTTGAACCTGTGGAGAGCTCGTCAATCAGCATGATGTTGATCTTTGACTCCCTGGCC 2631  
 3164 GTGATCTCTGGACCTCTGGAGAGCTCTGAGCAGGAGCCTCAACAGCCTGGCG 3223

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C	1	2202	80.5	2775	9	AY401469 Homo sapi
	2	1871.4	68.4	2507	9	AY401470 Pan trogl
	3	1796	65.6	2775	9	AY401471 Mus muscu
	4	565.8	20.7	3866	3	AK018177 Mus muscu
	5	529.4	19.3	532	6	CD3636011 56033904H
	6	529.4	19.3	596	6	CD3636012 56033928J
	7	517.4	18.9	530	6	CD3636012 56033904J
	8	501.2	18.3	2802	9	AY406491 Homo sapi
	9	491.6	18.0	2532	9	AY411747 Homo sapi
	10	476.4	17.4	3790	3	AK031655 Mus muscu
C	11	475.2	17.4	2791	9	AY406493 Mus muscu
	12	471.8	17.2	2532	9	AY411749 Mus muscu
	13	440	16.1	812	5	BX915627 BX915627
	14	434.2	15.9	2532	9	AY411748 Pan trogl
	15	386.2	14.1	896	5	BU447189 603214135
	16	372	13.6	445	5	BY291669 BY291669
	17	368	13.5	392	6	CD3636013 56033928H
	18	360.6	13.2	2802	9	AY406492 Pan trogl
	19	318	11.6	413	4	BM726542 UI-R-EJ0-
	20	312.6	11.4	567	2	BF390834 UI-R-CAL-
C	21	302.6	11.1	1843	3	BC034747 Homo sapi
	22	283.4	10.4	856	7	CNI164143 994266 MA
	23	283.2	10.4	390	5	BU729454 UI-R-CL1-
	24	282	10.3	378	4	BM702977 UI-R-CL1-





```
Db 2193 CCTCTGAGAAATTAAACCATTCAGTCTGCTGCGAGAAAGTCCGTTCTCCCGGTGTGGTG 2252
Qy 2214 CAGTAACCGCAGCCCTGCACTGTGCTTCTCCCTGGAGCGTTATACGCCCACTACCCAC 2273
Db 2253 CAGTAACCGCAGCCCTGCACTGTGCTTCTCCCTGGAGCGTTATACGCCCACTACCCAC 2312
Qy 2274 CCAGCTGTCTGCAAAATCTGCATTCGGCAGCTCAAAAGGCCATGAAAGATCTCCAGT 2333
Db 2313 CCAGCTGTCTGCAAAATCTGCATTCGGCAGCTCAAAAGGCCATGAAAGATCTCCAGT 2372
Qy 2334 GCAGACATCAATCTCAGAGAGTGAACGAGAAACCATCACTTCTTCGCAACAGAGGACAG 2393
Db 2373 GCAGACATCAATCTCAGAGAGTGAACGAGAAACCATCACTTCTTCGCAACAGAGGACAG 2432
Qy 2394 CACTTTCCTGCAAGACTGGCCCAAGCCTTCAAAATTCCTTACTCCATCAGACAGCG 2453
Db 2433 CACTTTCCTGCAAGACTGGCCCAAGCCTTCAAAATTCCTTACTCCATCAGACAGCG 2492
Qy 2454 GATTTGTGTACATTTGATATCCCAAGCCTTCAAAATTCCTTACTCCATCAGACAGCG 2513
Db 2493 GATTTGTGTACATTTGATATCCCAAGCCTTCAAAATTCCTTACTCCATCAGACAGCG 2552
Qy 2514 GAAAAACAGCATCAACAGGAATTTATCTTATTTGCTACACAAAGTAGCCCATCTGCTGT 2573
Db 2553 GAAAAACAGCATCAACAGGAATTTATCTTATTTGCTACACAAAGTAGCCCATCTGCTGT 2612
Qy 2574 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2633
Db 2613 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2672
Qy 2634 TGCCCTTGAAGAGATTGGGAGGACACACAGAACTCTCAAAATTCAGATCCCAAGCT 2693
Db 2673 TGCCCTTGAAGAGATTGGGAGGACACACAGAACTCTCAAAATTCAGATCCCAAGCT 2732
Qy 2694 TGATGAAGCCGACTTCAACTACAGCAGCAAAATGGACTCTAG 2736
Db 2733 TGATGAAGCCGACTTCAACTACAGCAGCAAAATGGACTCTAG 2775

RESULT 2
AY401470 2507 bp DNA linear GSS 12-DEC-2003
LOCUS Pan troglodytes HCM901 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY401470
VERSION AY401470.1 GI:39757459
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 2507)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2507)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
1..2507
```

```

/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>2507
/locus_tag="HCM901"

gene
ORIGIN

Query Match 68.4%; Score 1871.4; DB 9; Length 2507;
Best Local Similarity 83.3%; Pred. No. 0;
Matches 2124; Conservative 0; Mismatches 248; Indels 177; Gaps 3;

Qy 323 GTTTGAAGGTCCCGCAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGACTTCCATG 382
Db 1 GTTTGAAGGTCCCGCAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGACTTCCATG 60
Qy 383 GGCCCGAGGACTATTGGTGCAGTGTGTGGCGTGGAGCCAACCTGGGTACCTCCAAGACA 442
Db 61 GGCCCGAGGACTATTGGTGCAGTGTGTGGCGTGGAGCCAACCTGGGTACCTCCAAGACA 120
Qy 443 GGAAGCCTCTGTGCGCATAGCCTATTACGGAAGAACTTTGAACAAGACCCACAGGAA 502
Db 121 GGAAGCCTCTGTGCGCATAGCCTATTACGGAAGAACTTTGAACAAGACCCACAGGAA 180
Qy 503 GGGAAAGTCCCATTTGAAGGCATGATTGTACTGCTGCACTGCCGCCCAACAGAGGGAGTCCCTG 562
Db 181 GGGAGGTTCCTCATTTGAAGGCATGATTGTACTGCTGCACTGCCGCCCAACAGAGGGAGTCCCTG 240
Qy 563 CTGCCGAGGTGGAATGGCTGAAATAATCAAGAGCCCATTTGACTCTGAAACAAGACGAGAA 622
Db 241 CTGCNNNGTGGAAATGGCTGAAATAATCAAGAGCCCATTTGACTCTGAAACAAGACGAGAA 300
Qy 623 TTGACAACGAGGTGACCAATACCTGATCATACGAGCAGGACCGGCTCTCGGACTCAGGAA 682
Db 301 TTGACAACGAGGTGACCAATACCTGATCATACGAGCAGGACCGGCTCTCGGACTCAGGAA 360
Qy 683 ATTACACCTGCACTGCGAGCCCAACATCGTGGCTAAGAGGAGAACGCTGCGGCACATGTTG 742
Db 361 ATTACACCTGCACTGCGAGCCCAACATCGTGGCTAAGAGGAGAACGCTGCGGCACATGTTG 420
Qy 743 TGGTCTACGTGGATGGGAGCTGGGAAAGTGTGGAGCGAAATGGTCCGTCTGCAGTCCAGAGT 802
Db 421 TGGTCTACGTGGATGGGAGCTGGTCTTCTGGAGCAGAGTGTGAGCTGCAATGTTGCTG 480
Qy 803 GTG-----AACATTTGCGGATCCGGAGTGCACAGCACACCCCGAGAAATGGGG 853
Db 481 GTGCTAGAGGATGGCAGAAACGTTCCCGGACCTGCACCAACCCAGCTCTCTCAATGGTG 540
Qy 854 GCAAAATCTGTGAAGTCTAAGCCAGGAATCTGAAAACTGCAC----- 896
Db 541 GGGCCTTTTGTGAGGAAATGTTCAGTGCAGAAATAACCTGCACTTCTTTTGTCTGNNN 600
Qy 897 ----- 896
Db 601 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 660
Qy 897 -----AGATGGTCTTT 907
Db 661 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720
Qy 908 GCATCTAGATAAAAAACCTTTCATGAAATAAAAAACCCAAAGCATTTGAGAAATGCCAGCG 967
Db 721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780
Qy 968 ACATTCCTTTTGTACTCGGGCTTGGGCTGCTGCCGTGCTGGCGGTGGAGTCTCTGTCATTG 1027
Db 781 ACATTCCTTTTGTACTCGGGCTTGGGCTGCTGCCGTGCTGGCGGTGGAGTCTCTGTCATTG 840
Qy 1028 GTGTCAACCTTTTACAGACGAGCAGAGTGAATATGCGGTGAGCGTCAATGACTTCTTCTG 1087
Db 841 GTGTCAACCTTTTACAGACGAGCAGAGTGAATATGCGGTGAGCGTCAATGACTTCTTCTG 900
Qy 1088 CATTTGACGGTGGCTTCCAGACCTTCAATTTCAAAACAGTCCGTCAAGCCCAAGAAATATCA 1147
Db 1147 CATTTGACGGTGGCTTCCAGACCTTCAATTTCAAAACAGTCCGTCAAGCCCAAGAAATATCA
```

Db	901	CATTGACAGGTGGCTTCAGACACTTCAACTTCAAAACAGTCCGTCAA	947
Qy	1148	TGGAACATAATGATACAAAGAAAATCCCTTTGGTAACTCCCTGCTCCTGAATTTCTGCCATGC	1207
Db	948	-----GNNNACTCCCTGCTCCTGAAATTCGGCCATGC	978
Qy	1208	AGCCAGATCTGACAGTGAGCGGACATACAGCGGACCCATCTGCTCGAGGACCTCTCG	1267
Db	979	AGCCAGATCTGACAGTGAGCGGACATACAGCGGACCCATCTGCTCGAGGACCTCTCG	1038
Qy	1268	ACAAGAGGCTCATGACAGAGTCCTCACTCTTTAAACCCCTTTGTCCGACATCAAAAGTGAAG	1327
Db	1039	ACAAGAGGCTCATGACAGAGTCCTCACTCTTTAAACCCCTTTGTCCGACATCAAAAGTGAAG	1098
Qy	1328	TCCAGAGCTCGTTTCATGGTTTCCCTGGGAGTGTCTGAGAGGCTGAGTACACGGCAAGA	1387
Db	1099	TCCAGAGCTCGTTTCATGGTTTCCCTGGGAGTGTCTGAGAGGCTGAGTACACGGCAAGA	1158
Qy	1388	ATCAATCCAGGACTTTTCCCATGGAAAACAACACAGCTTTAGTACAAATGCATCCCCAGAA	1447
Db	1159	ATCAATCCAGGACTTTTCCCATGGAAAACAACACAGCTTTAGTACAAATGCATCCCCAGAA	1218
Qy	1448	ATAAAATGCCCTACATCAAAATCTGTCACTCCTCCCAACAAGACAGAACTGAGGACAA	1507
Db	1219	ATAAAATGCCCTACATCAAAATCTGTGATCACTCCCAACAAGACAGAACTGAGGACAA	1278
Qy	1508	CTGGTGTCTTTGGCCATTATAGGGGGGGCTTAGTAAATGCCAAATACAGGGGTGAGCTTAC	1567
Db	1279	CTGGTGTCTNNNGCCATTATAGGGGGGGCGNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1338
Qy	1568	TCATACCACACGGTGCCATCCACAGAGAGAAATCTTGGGAGATTATATGTCCATCAACC	1627
Db	1339	NN	1398
Qy	1628	AAGGTGAACCCAGCTCAGATGGCTCTGAGGTGCTCTGAGTCTCTGAGTCTGAAATCACT	1687
Db	1399	NNNNNNNNNNNNCTCCAGTCAGATGGCTCTGAGGTGCTCTGAGTCTGAAATCACT	1458
Qy	1688	GTGCTCTCCAGACATGATCGTCACCACTCCCTTTGCAATTGACCATCCGCACTGTGCAG	1747
Db	1459	GTGCTCTCCAGACATGATCGTCACCACTCCCTTTGCAATTGACCATCCGCACTGTGCAG	1518
Qy	1748	ATGTCAGTCTGAGCATTTGGAATATCAATTTAAAGAGAGGACACAGAGGGCAAAATGGG	1807
Db	1519	ATGTCAGTNNAGCATGGAATATCAATTTAAAGAGAGGACACAGAGGGCAAAATGGG	1578
Qy	1808	AGGAAGTGATCTAGTGGAGATGAATCATCTCTGTACTGCTTTTGGACCCCTTTG	1867
Db	1579	AGGAAGTGATCTAGTGGAGATGAATCATCTCTGTACTGCTTTTGGACCCCTTTG	1638
Qy	1868	CGTGTCAATGCTCTCTGGACAGCTTTGGGACCTATGGCTCACTGGAGAGCCAAATCACAG	1927
Db	1639	CATGTCAATGCTCTCTGGACAGCTTTGGGACCTATGGCTCACTGGAGAGCCAAATCACAG	1698
Qy	1928	ACTGTGCGGTGAAGCAACTGAAGTGGGGTTTTTGGCTGATGCTGCTGTAATCTCCCTGG	1987
Db	1699	ACTGTGCGGTGAAGCAACTGAAGTGGCGGTTTTTGGCTGATGCTGCTGTAATCTCCCTGG	1758
Qy	1988	ATTACAACTTGAGAGTTTACTGTGTGACAATACCCCTTGTCATTTTCAAGAGTGGTTT	2047
Db	1759	ATTACAACTTGAGAGTTTACTGTGTGACAATACCCCTTGTCATTTTCAAGAGTGGTTT	1818
Qy	2048	CAGATGAAGGCAATCAAGGTGGAAGCTCTCTGGAAGAAACAAATTTGCTGATTTCAAAG	2107
Db	1819	CAGATGAAGGCAATCAAGGTGGAAGCTCTCTGGAAGAAACAAATTTGCTGATTTCAAAG	1878
Qy	2108	GGATACCTTTAGTCTTCAGATTTCTGCTCTTGATATTCGCCCAATCTCTGAGGAATTA	2167
Db	1879	GGATACCTTTAGTCTTCAGATTTCTGCTCTTGATATTCGCCCAATCTCTGAGGAATTA	1938
Qy	2168	AACCAATTCATGCTGCCAGGAAGTCCGGTTCTCCCGCTGTGGTGCAGTAAACGGCAGC	2227
Db	1939	AACCAATTCATGCTGCCAGGAAGTCCGGTTCTCCCGCTGTGGTGCAGTAAACGGCAGC	1998

QY	2228	CCCTGCACTGTGCTCTTCCCTCGAGGCGTTATACGCCCACTACACCCAGCTGTCCTGCA	2287
DB	1999	CCCTGCACTGTGCGCTTCTCCCTCGAGGCGTTATACGCCCACTACGCCCACTGTCCTGCA	2058
QY	2288	AAATCTGCATTTGGCGAGCTCAAAAGGCCATGAAACAGATCTCTCCAAAGTGCAGACATCAATCC	2347
DB	2059	AAATCTGCATTTGGCGAGCTCAAAAGGCCATGAAACAGATCTCTCCAAAGTGCAGACATCAATCC	2118
QY	2348	TAGAGAGTGAAACGAGAAACCATCACTTTCTTCGCAACAGAGGACAGCACTTTTCCTGTCAC	2407
DB	2119	TAGAGAGTGAAACGAGAAACCATCACTTTCTTTGCAACAGAGGACAGCACTTTTCCTGTCAC	2178
QY	2408	AGACTGGCCCCCAAGCCCTTCAAAATTCCTTACTCCATCAGACAGCGGATTTGTGCTACAT	2467
DB	2179	AGACTGGCCCCCAAGCCCTTCAAAATTCCTTACTCCATCAGACAGCGGATTTGTGCTACAT	2238
QY	2468	TTGATACCCCCCAATGCCAAAGGCAAGACTGGCGAGATGTTAGCACAGAAAAACAGCATCA	2527
DB	2239	TTGATACCCCCCAATGCCAAAGGCAAGACTGGCGAGATGTTAGCACAGAAAAACAGCATCA	2298
QY	2528	ACAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCTGCTGTCTATTTTGAACCTGT	2587
DB	2299	ACAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCTGCTGTCTATTTTGAACCTGT	2358
QY	2588	GGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCGCTGTGCCCTTTGAAGAGA	2647
DB	2359	GGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCGCTGTGCCCTTTGAAGAGA	2418
QY	2648	TTGGGAGGACACACACGAAACTCTCAAAATTTTCAGAAATCCAGACTCCAGCTGTAAGACCGACT	2707
DB	2419	TTGGGAGGACACACACGAAACTCTCAAAATTTTCAGAAATCCAGACTCCAGCTGTAAGACCGACT	2478
QY	2708	TCAACTACAGCGCAAAATGGCACTTAG	2736
DB	2479	TCAACTACAGCGCAAAATGGCACTTAG	2507

RESULT 3	AY401471	2775 bp	DNA	linear	GSS 12-DEC-2003
LOCUS	Mus musculus HCN0901 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
DEFINITION	AY401471				
ACCESSION	AY401471.1	GI:39757460			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2775)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrlera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Infering nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2775)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrlera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment				
FEATURES	Location/Qualifiers				
source	1..2775				
	/organism="Mus musculus"				
	/mol type="genomic DNA"				

gene		/db_xref="taxon:10090"		QY	
ORIGIN		<1..>2775		Db	
		/locus_tag="HCM0901"			
Query Match 65.6%; Score 1796; DB 9; Length 2775;					
Best Local Similarity 79.2%; Pred. No. 0;					
Matches 222; Conservative 0; Mismatches 340; Indels 243; Gaps 3;					
QY	100	CGAGGAACATGACAAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCTCGGACACTG	159	892	TGCACAGATGGCTTTGGCATCTCTAGATAAAAAACCTCTTTCATGAATAAAAAACCCCAAGC
Db	46	CCAGGAGCCGATGGCAGTGAATTTCTCCCGACTCTATCCCATCTGCCCTTGGAAACGCTG	105	1006	TGCACAGATGGTCTCTGCATTTAG-----GC
QY	160	CCTCATTTATAGAGGAGCCAGATGATGCTTATATATCAAGAGCAACCTATTGCACTC	219	952	ATTGAGAATGCCAGCAGCATTTGCTTTGTACTCGGGCTTGGGTGCTGCCGCGTCTT
Db	106	CCTCATTTATCAGGAGGCCGGAAGATGATATACATCATCAAGAGCAACCCGATTTGCACTC	165	1033	ATTGAGAATGCCAGCAGCATTTGCTTTGTACTCGGGCTTGGGTGCTGCCGCGTGTAGCTGT
QY	220	AGGTGCAAGCGAGGCCAGCATGTCAGATATTTCTCAAAATGCAACGGCGAGTGGGTCCAT	279	1012	GCAGTCTGGTCAATTTGGTGTCAACCTTTACAGACGAGGACAGAGTACTATAGCGGTGGAC
Db	166	AGGTGCAAGCGAGGCCAGCATGTCAGATATTTCTTCAAAATGCAATGGGAGTGGGTCCAT	225	1093	GGGTCTGGTCAATTTGGTGTCAACCTTTACAGACGAGGACAGAGTACTACGGAGTGAT
QY	280	CAGAACGAGCACTCTCTGAAGAGACTCTGGAAGAGAGTCTGGAAGAGTCTGAGTCTGAG	339	1072	GTCAATGACTCTTTTGCATTTGACAGTGGCTTCCAGACCTTTCAACTTTCAAAAAGTCCGT
Db	226	CAGAAATGAACATGTCTCCAGGAGAGCTCTGGAAGAGTCTGAGTCTGAGTCTGAGTCTGAG	285	1153	GTCAATGACTCTTTTGCATTTGACAGTGGCTTCCAGACCTTTCAACTTTCAAAAAGTTCGT
QY	340	GTGTTTCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCGAGGACTATTGG	399	1132	CAAGCCAGAATATCATTGGAACTAATGATACAAGAAAAATCCCTTTGTTACTCTCCCTGCTC
Db	286	GTGTTTATCAATGTCACAGGAGCAAGTGGAGGACTTCCATGGGCCGAGGACTACTGG	345	1213	CAA-----GGAATTTCTCTACTA
QY	400	TGCCAGTGTGTGGGTGGAGCCACTGGGTACCTCCAAAGAGCAGGAGGCTCTGTGGCC	459	1192	CTGAATTTCTGCGCATGAGCCAGATCTGACAGTGGCGGACATACAGCGGACCCATCTGT
Db	346	TGCCAGTGTGTGGGTGGAGCCACTGGGTACCTCCAAAGAGTGGAGGCTCTGTGGCC	405	1231	CTGAATCTGCGCATGAGCCAGATCTGACTGTGAGCGGACATACAGCGGCGCCATCTGT
QY	460	ATAGCCTATTATCGGAAAACTTTTGAACAAAGATCCCAAGGAGGAGTTCCTCATTTGAA	519	1252	CTGCAGGACCTCTCGGACAAAGGAGCTCATGACAGAGTCTCTCACTCTTAAACCTTTGTGCG
Db	406	ATAGCCTATTATCGGAAAACTTTTGAACAAAGATCCCAAGGAGGAGTTCCTCATTTGAA	465	1291	CTGCAGGATCCGCTCGCAAGGAGCTCATGACAGAGTCTCTCACTCTTCAATCTCTTATCT
QY	520	GGCATGATTGTAATGCACTGCGGCCACAGAGGAGTCCCTGCTGCGAGGTGGAAATGG	579	1312	GACATCAAAAGTGAAGTCCAGAGTCTGTTTCATGGTTTTCCCTGGGAGTGTCTGAGAGAGCT
Db	466	GGCATGATCGTGTGATTGTCGCGCCAGAGGAGTTCACAGCAGCAGAGTGGAAATGG	525	1351	GACATCAAAAGTGAAGTCCAGAGTCTATTTATGTTTTCTCTGGAGTGTCTGAGAGAGCG
QY	580	CTGAAAAATGAAGAGCCATTGACTCTGAAACAAAGACGAGAGCAATTTGACACAGGCTGAC	639	1372	GAGTACCAACGCGGAAGATCAATTCAGGACTTTTCCCATGGAACAAACCAAGCTTTAGT
Db	526	CTGAAAAATGAAGAGCCATTGACTCTCGAAACAAAGATGAGAAATTTGACACAGGCTGAC	585	1411	GAGTACCAACGCGGAAGATCAATTCAGGACTTTTCCCATGGAACAAACCGGGATTCAGT
QY	640	CATAACCTGATCATCAGGAGGACGCGCTCTCGGACTCAGGAAATTCACCTGATGGCA	699	1432	ACAAATGCAATCCCAAGAAATATAATGCCCTACATCCAAATCTGTCTCATCTCCCAAGG
Db	586	CATAACCTGATCATCAGAGGACGCGCTCTCAGACTCAGGAAATTCACCTGATGGCA	645	1471	ACAAATGCAATCCCAAGAAACAAACGCGGTACATCCAAATCTGTCTCATCTGCCGCAAGG
QY	700	GCCAAACATCGTGGTAAGAGGAGAACCTGTGCGGCCACTGTTGTGGTCTAC-----	750	1492	ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAAT
Db	646	GCCAAACATCGTGGCCAAAGAGGAGGAGCTCTCAGCAATCTGTGGTGTCTACGTGATGGA	705	1531	ACAGAGCTGAGGACAACTGGTGTCTTTGGGCCATTTAGGGGGACGCTTAGTAAATGCCAAAT
QY	751	-----	750	1552	ACAGGGGTGAGCTTACTCATACCAACGCGTGGCATCCACAGAGGAGAAATCTTTGGGAGATT
Db	706	GGCTGGTCTTCTCGACAGAGTGGTACGCTGCAATGTTGCGTGTGGTAGAGATGGCAG	765	1591	ACAGNN
QY	751	-----	750	1612	TATATGTCCATCAACCAAGGTGAAACCCAGCTCCAGTCCAGTCCAGTCCAGTCCCTG
Db	766	AAACGTTCCCGGACCTGCACCAACCCCGCTCTCTCAATGGTGGGCGCTTTTGTAGGGA	825	1651	NN
QY	751	-----	750	1672	AGTCTGAAAGTCACTGTGGTCTCCAGACATGATCGTCCACCATCCCTTTGCAATTCAGCC
Db	826	ATGTGAGTGGAAAAATAACCTGCACTGCTCTTTTGTCTCTGATGGCAGCTGGGAATG	885	1711	AGTCTGAAAGTCACTGTGGGCTCCAGATATGCTTGTCACAACTCCCTTTGGCGCTGACC
QY	772	TGAGCGAATGGTCCGCTCTGAGTCCAGAGTGGAAACATTTTGGGATCCGGGAGTGCACA	831	1732	ATCCGCACTGTGAGATGTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACA
Db	886	TGAGTGAATGGTCTGAGTCTGACGCCAGAGTGTGAAACATCTTCGTATCCGTGATGGACA	945	1771	AGTCTGAAAGTCACTGTGGGCTCCAGATATGCTTGTCACAACTCCCTTTGGCGCTGACC
QY	832	GCACACCCCGGAGAAATGGGGCAAAATTTCTGTAAGTCTTAAGCCAGGAAATCTGAAAC	891	1792	ATCCCGCACTGTGACAGATGTCTGAGTTCAGCATTTGGAATATCCATTTAAAGAGAGGACA
Db	946	GCTCCACCCCAAGAAATGGGGCAAAATTTCTGTAAGTCTTAAGCCAGGAAATCTGAAAC	1005	1831	CAGCAGGCAATGGGAGGAGTGTGATGAGTGGAGAGTGTGATGAGTGGAGTGTGATGTC

[illegible]

## RESULT 4

AK018177	AK018177	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330415B02 product:TRANSMEMBRANE RECEPTOR UNC5H2 homolog (Rattus norvegicus). full insert sequence.	3866 bp	linear	HTC 03-APR-2004
LOCUS					
DEFINITION					

**ACCESSION**

VERSION AK018177.1 GI:12857775

**KEYWORDS** HTC; CAP trapper.

**SOURCE** *Mus musculus* (house mouse)

ORGANISM

. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

**AUTHORS** Carninci, P. and Hayashizaki, Y.

**TITLE** High-efficiency full-length cDNA cloning

JOURNAL Meth. En

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

**AUTHORS** Carninci

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

**TITLE**  
**JOURNAL**

COMMENT

FEATURES  
source

```
/db_xref="PANTOM DB:6330415E02"  
/db_xref="taxon:10090"  
/clone="6330415E02"  
/sex="male"  
/tissue types="medulla oblongata"  
/clone_lib="RIKEN full-length enriched mouse cDNA library"  
/dev_stage="adult"  
417..3254  
CDS  
/note="unnamed protein product; TRANSMEMBRANE RECEPTOR  
UNC5H2 homolog [Rattus norvegicus] (SPTR|008722, evidence:  
FASTY, 96.5%ID, 100%length, match=2835)  
putative"  
/codon_start=1  
/protein_id="BAB31108.1"  
/db_xref="GI:12857776"  
/translation="MRARGSVRSALLALLLLWDPTPLSLAGVDSAGQVLPDSYSPAPA  
EQLPYFLEPQDAIYVKNKGVRLHRAFAFATQIYFKNGEWSQNDHVTQESLDEATG  
LRVEQIEVSRQVQELFGLDWCQVAMSSGTTKSRRAVIRIAYLRKNFDQRLP  
AKEVPIDHEVLQCRPEGPVPAEVEWLNKVEDIDPAQDTPFLITDHNLIIRQARLS  
DTANYTCVAKNIIVAKRRSTAAIVIVVNGWSSWAESWSPSCNRCRGWQKRTICNP  
APLNGAFCEGQAFQCTACTTVCVGDGAWTEWSKASCTECAHWSRECMAPPQNG  
GRDCSTLDSKCTDGLCVLNQRTLNDPKSHPLETSGDVALYAGLVPAVFVVAVLM  
IYRGPVVALQDSADKIPMTNSPLDPLPSIKIVYNSSTIGSGGLADGADLGLVLP  
AEGVIVYRNCRDFDITDSAAALGTFPVNFKTARPNNPOLLGHPSPDLPASAG  
GTYGPDFSRDTHLHRSASLGSQHLGLPRDPSVSVSGTFGLGRLSLPRTGVSL  
VPNGAIPQGFYDLYLHINKAESTLPLSEGSQTVLSPSVCTGTLGLCRPVVLTVP  
CAEVIADMTIFQKTHQHQHWEVVTLDSEETLNTPCYQLEAKSCHILLDQIGSVYF  
MGYSRSVAVRQLQAIAPALCTSLYSRLVYCLEDTVALKEVLESLHCTFLYVE  
EKPRLFPKSLHSLHDI PHAHRSLKLLAKYQBIPIFYHWNQSORALHCTFLYER  
HSLASTEFTKVCVROVEGBOIFOLHTTLAETPAGSLDALCSAPGNATITOLGPVAF  
KIPLSIROKICSSLDAPDSRGNDRWLLAQKLSMDRYLNPATKASPTGVILLDWEARQ  
QDDGLNSLASALEEMKSEMLVAMATDGC"
```

## ORIGIN

```
Query Match 20.7%; Score 565.8; DB 3; Length 3866;  
Best Local Similarity 54.2%; Pred. No. 81e-154;  
Matches 1541; Conservative 0; Mismatches 1057; Indels 243; Gaps 10;
```

```
Qy 25 GGCGGGCGGAGGGCGCGCGTGGCTCCCGTGGCTGGGGCTGGCTTCTGGGGCGCA 84  
Db 423 GCCCGAGCGGGTGGCGAGCGCGTCTGCTGGCGCTGCTGCTTTGCTGGGATCCGACA 482  
Qy 85 GGGACCGCGCTGCCGAGAACTGACAAATGGCGAGCCCTTCCGNAATCCATCCCATCA 144  
Db 483 CCGAGCCTAGCAGCGCTGTGCTCTGGCGCAGGTGCTCCAGACTCTTACCATCAGCC 542  
Qy 145 GCTCCTGGGACACTGCTCTATTCATAGAGGACGACATGATGCTTATATTAACAAGAGC 204  
Db 543 CTTGGGAGCAGTGGCTGCTACTTCTATTTGGAGCCACAGAGCGCTACATCGTAAGAAC 602  
Qy 205 AACCTTATGCACTCAGGTCAAAGCGAGGCCAGCCATGAGATATTTCTCAAAATGCAAC 264  
Db 603 AAGCCAGTGAACCTGCACTGAGAGCGCTTCCCTGCCACGAGATCTACTTCAAGTGAAT 662  
Qy 265 GCGAGTGGGTCCATCAGACGAGCAGCTCTCTGAGAGACTCTGGACGAGAGCTCAGGT 324  
Db 663 GCGAGTGGGTGAGCCAGATGACCACTCACAAGAGAGCGCTGGATGAGCCACAGGC 722  
Qy 325 TTGAAGGTCCGCAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGG 384  
Db 723 TTGGGGTGGAGGTGAGATCGAGTGTACGGCAGCAGTGGAGGAACTCTTCCGG 782  
Qy 385 CCCGAGGACTATTGGTSCCAGTGTGGCGTGGAGCCACCTGGGTATCTTCAAGAGCAGG 444  
Db 783 CTGAGGACTACTGGTCCAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 842  
Qy 445 AAGCCCTCTGGGCATAGCTTATTACGGAAACCTTTGAAACAGACCCACAGGAGG 504  
Db 843 CGAGCCTACATCCGCAATTGCTACTTGGCAAGAACTTTGACGAGGAGCTCTGGCCAA 902  
Qy 505 GAAGTTCCTCAATGAAGCATGATTGTACTGCACCTGCCGCCACACAGAGGAGTCCCTGCT 564  
Db 903 GAGTACCTTGGATCATGAGGTCTCTTCTGAGTGGCCGCCACCGGAGGAGTGCCTGTG 962
```



Qy	1456	CCCTACATCCAAATCTGTCTATCACTCCCAACAAGACAGAACTGGAGCAAACTGGTGTC	1515
Db	2001	CTTGGTTCCCAAGCACTCTGGGCGCTACCTCGGACGCCAGACAGCAGTGTGAGCGGCACC	2060
Qy	1516	TTTGGCCATTTAGGGGGCGCTTAGTAATGCAAAATACAGGGGTGAGCTTACTCATACCA	1575
Db	2061	TTTGGTTGCCGTGGGAGAAGGCTGAGCCTCCCGGCACAGGGGTGACGCTGTTGGTACCA	2120
Qy	1576	CACGGTGCATCCCAAGAGGAAATCTTTGGAGATTTATATGTCCATCAACCAAGGTGAA	1635
Db	2121	AA TGAGGCCATTCCCAAGGCAAGTTCTATGACCTGTATCTAATATCAACAGGCCGAA	2180
Qy	1636	CCCAGCCTC---CAGTCAGATGGCTCTGAGTGTCTCTGAGTCTCTGAAGTCACTGTGGT	1692
Db	2181	AGCACCTCCACTTTCAGAAAGTTCCAGACAGTATTGAGCCCTCGGTGACCTGTGGG	2240
Qy	1693	CCTCCAGACATGATCGTCAACACTCCCTTTTGCAATTGACCATCCGGACTGTGCAGATGTC	1752
Db	2241	CCCA CAGGCCCTACTCTGTGCGCGCCCTGTGTCTCTACCGTGGCCCACTGTGTCTGAATC	2300
Qy	1753	AGTTCTGAGCATTGGAAATATCCATTTAAAGAAGAGGACACAGCAGGGCAAAATGGGAGAA	1812
Db	2301	ATCGCTGGAGCTGGATCTTTTCAGCTCAAGACCAGGCCCATCAGGGCCACTGGAGGAG	2360
Qy	1813	GTGATGTCAGTGGAGAATGAATC-----TACATCTCTGTTACTGCTCTTTTGGACCCCTTT	1866
Db	2361	GTGTGACCTTGGATGAGGAGACCTCAACACACCCCTGTCTACTGCCAGCTGGAGGCTAAG	2420
Qy	1867	GCGTGTCAATGTCTCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGGCCAAATCACA	1926
Db	2421	TCTTCGCCACATCTCTGTGGACAGCTGGGTTCCTACGTATTCATGGGCGAGTCTACTCT	2480
Qy	1927	GACTGTGCCGTGAAGCAACTGAAAGTGGCGGTTTTTGGCTGCATGTCTCTTAATCCCTTG	1986
Db	2481	CGTCTGCACTCAAGCGGCTCCAGCTGGCCATCTTGGCCCCAGCCCTCTGCACCTCCCTG	2540
Qy	1987	GATTACAACTTGAGAGTTTACTGTGTGGACAAATACCCCTTGTGCAITTCAGGAAGTGTT	2046
Db	2541	GAGTATAGCCTCAGGGTCTACTGTCTGGAGGACACACCTGTAGCACTGAAAGGAGTCTTG	2600
Qy	2047	TCAGATGAAGGATCAAGTGTGACAGCTCTCTGGAAGAACAAATTCGTGCAATTTCAAA	2106
Db	2601	GAGCTGGAGAGGACTCTGGGTGGCTACTTGGTGGAGGAGCCAAAGCCTTTGCTCTTTAAG	2660
Qy	2107	GGCAATACCTTTAGTCTTCAGATTCTGTCTTTGATATCCCCCAATCTCTCTGAGAAATT	2166
Db	2661	GACAGTTACCAAACTACGCTCTCCCTCAATGACATCCCCCACTGCCCACTGGAGAGC	2720
Qy	2167	AAACCAATCACTGCCCTGCCAGGAAGTCCCGTTCTCCGGCTGTGTGTCAGTAACCGGCAG	2226
Db	2721	AAACTACTGCCCAAGTACCAAGGAGATTCCCTTCTACCACTCTGGAAATGGCAGCCAGAGA	2780
Qy	2227	CCCTGCACTGTGCTTCTCCTGTGAGCGTTTATAGGCCCACTAACCCAGCTGTCTCTGC	2286
Db	2781	GCCTTGCACTGCACTTTACCCCTGGAGAGCATAGCCTGGCTCTCCACGGAGTTTCACTGT	2840
Qy	2287	AAAATCTGCATTTCGGCAGCTCAAAAGGCCATGAACAGATCTCTCAAGTGCAGACATCAATC	2346
Db	2841	AAGGTCTGCTGTGGCAGAGTTCGAAGGGGAAGGCCAGATTTTCAGCTGCACACACGTTG	2900
Qy	2347	CTAGAGAGTGAACGAGAAACCAT---CAGTTTTCTTGGCACAGAGGACAGCACTTTCCCT	2403
Db	2901	GCCGAGAGGCTCTGCTGCCCTCCGTGGATGTCTCTGTCTTGCCCCGGGCAATGCCATCACC	2960
Qy	2404	GCACAGACTGGCCCCAAGCCTTCAAAATTTCCCTACTTCATCAGACAGCGGATTTGTGCT	2463
Db	2961	ACCACGTGGGACCTATGTCTTTCAGATACCCCTGTCTCATTCGCCCAAAAGATCTGCAGC	3020
Qy	2464	ACATTTGATACCCCAATGCAAAAGCAAGGACTGGCAGATGTTTACACAGAAAAACAGC	2523
Db	3021	AGCCTGGAACCCCCCGACTCCCGGGGCAACGACTGGAGGCTGTGTGGCGAAGAGTGTCTC	3080
Qy	2524	ATCAACAGGAATTTATCTTATTTTCGTACACAAAGTAGGCCCATCTCTGTCTCAATTTTGAAC	2583

Db	3081	ATGACCGGTACCTAAACTACTTTCGCCACCAAGCTAGTCCACAGGTGTCATCTTAGAC	3140
Qy	2584	CTGTGGGAAGCTCGTCATCAGCATGATGGTACTTGTGACTCCCTGGCCTGTGCCCTTGAA	2643
Db	3141	CTCTGGGAAGCTCGGCACACAGGATGACGGGGACCTCAACAGCCCTGGCCAGTGCCTTGGAG	3200
Qy	2644	GAGATTGGGAGGACACACACG	2664
Db	3201	GAGATGGCAGAGTGGATG	3221
RESULT 5			
LOCUS	CD636011	532 bp	mRNA linear EST 12-JAN-2004
DEFINITION	56033904H1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD636011		
VERSION	CD636011.1	GI:40284278	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 532)		
TITLE	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes		
JOURNAL	Genomics 84 (1), 205-210 (2004)		
COMMENT	Contact: Fu GK Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Email: gfu@incyte.com.		
FEATURES	location/Qualifiers		
source	1..532		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone_lib="FLP"		
	/note="Vector: pDrive Cloning Vector"		
ORIGIN			
Query Match	19.3%;	Score 529.4;	DB 6; Length 532;
Best Local Similarity	99.8%;	Pred. No. 1.9e-143;	
Matches 530;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
Qy	1151	AACTAATGATACAGAAGAAATTCCTTTGGTAACTCCCTGCTCTGTAATTCCTGCAATTCGCGATCGAGC	1210
Db	1	AACTAATGATACAGAAGAAATTCCTTTGGTAACTCCCTGCTCTGTAATTCCTGCAATTCGCGATCGAGC	60
Qy	1211	CAGATCTGACAGTGAGCCGGGACATACAGCGGACCCATCTGTCTGCAGGACCCCTCTCGACA	1270
Db	61	CAGATCTGACAGTGAGCCGGGACATACAGCGGACCCATCTGTCTGCAGGACCCCTCTCGACA	120
Qy	1271	AGGAGCTCATGACAGAGTCTCTACTCTTTAAACCCCTTTGTCGGACATCAAAAGTGAAGTCC	1330
Db	121	AGGAGCTCATGACAGAGTCTCTACTCTTTAAACCCCTTTGTCGGACATCAAAAGTGAAGTCC	180
Qy	1331	AGAGCTCGTTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAACGCGCAAGAATC	1390
Db	181	AGAGCTCGTTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAACGCGCAAGAATC	240
Qy	1391	ATTTCAGGACTTTTCCCATGGNAACAACACAGCTTTTAGTACAAATGCATCCCGAANAATA	1450
Db	241	ATTTCAGGACTTTTCCCATGGNAACAACACAGCTTTTAGTACAAATGCATCCCGAANAATA	300
Qy	1451	AAATGCGCTACATCCAAAATCTGTCTCATCACTCCCAACAAGGACAGAACTGAGGACAACCTG	1510
Db	301	AAATGCGCTACATCCAAAATCTGTCTCATCACTCCCAACAAGGACAGAACTGAGGACAACCTG	360
Qy	1511	GTCTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTGAGCTTACTCA	1570
Db	361	GTCTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTGAGCTTACTCA	420



```
QY 1571 TACCACAGGTGGCCATCCACAGAGAGAAATCTTTGGGAGATTATATCTCCATCAACCAAG 1630
Db 421 TACCACAGGTGGCCATCCACAGAGAGAAATCTTTGGGAGATTATATCTCCATCAACCAAG 480
QY 1631 GTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAG 1681
Db 481 GTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAG 531

RESULT 6
CD636014/c
LOCUS CD636014 596 bp mRNA linear EST 12-JAN-2004
DEFINITION 54033928J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD636014
VERSION CD636014.1 GI:40284281
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 596)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
source
location/Qualifiers
1..596
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 19.3%; Score 529.4; DB 6; Length 596;
Best Local Similarity 93.1%; Pred. No. 2e-143;
Matches 593; Conservative 0; Mismatches 1; Indels 43; Gaps 2;

QY 1046 GGAGCCAGAGTGACTATGGGTGAGCGTCAATTGACTCTTCTGCAATGACAGGTGGCTTCC 1105
Db 595 GGAGCCAGAGTGACTATGGGTGAGCGTCAATTGACTCTTCTGCAATGACAGGTGGCTTCC 536
QY 1106 AGACCTTCAACTTCAAAACAGTCGGTCAAGCCAGATATCATGGAATCAATGATACAAG 1165
Db 535 AGACCTTCAACTTCAAAACAGTCGGTCAA----- 507
QY 1166 AAAAATCCTTTGGTAACTCCCTGCTCTGCAATCTGCCATGCGACGAGATCTGACAGTGA 1225
Db 506 -----GGTAACTCCCTGCTCTGCAATCTGCCATGCGACGAGATCTGACAGTGA 458
QY 1226 GCGGACATACAGCGGACCCATCTGTCTGCAAGACCTCTTGGACAAGAGCTCATGACAG 1285
Db 457 GCGGACATACAGCGGACCCATCTGTCTGCAAGACCTCTTGGACAAGAGCTCATGACAG 398
QY 1286 AGTCCTCAC-TCTTTAAACCTTTGTCCGACATCAAGTGAAGTCCAGAGCTCGTTCAATG 1344
Db 397 AGTCCTCACGCTTTTAAACCTTTGTCCGACATCAAGTGAAGTCCAGAGCTCGTTCAATG 338
QY 1345 GTTTCCCTGGAGTGTCTGAGAGAGCTGAGTACCACCGCAAGATCAATCCAGGACTTTT 1404
Db 337 GTTTCCCTGGAGTGTCTGAGAGAGCTGAGTACCACCGCAAGATCAATCCAGGACTTTT 278
QY 1405 CCCCATGGAAACAAACACAGCTTTTGTACATGATCCCGAATAAAATGCCCTACATC 1464
Db 277 CCCCATGGAAACAAACACAGCTTTTGTACATGATCCCGAATAAAATGCCCTACATC 218
QY 1465 CAAATCTGTATCATCTCCCCCAAGAGCAGAACTGAGGACAACTGGTGTCTTTGGCCAT 1524
```

```
Db 217 CAAATCTGTATCATCTCCCAACAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCAT 158
QY 1525 TTAGGGGGGGCGCTTAGTAAATGCAAAATACAGGGGTGAGCTTACTCATACACAGCGTGCC 1584
Db 157 TTAGGGGGGGCGCTTAGTAAATGCAAAATACAGGGGTGAGCTTACTCATACACAGCGTGCC 98
QY 1585 ATCCACAGAGGAGAAATCTTTGGGAGATTATATGTCCATCAACCAAGGTACCCAGGCTC 1644
Db 97 ATCCACAGAGGAGAAATCTTTGGGAGATTATATGTCCATCAACCAAGGTACCCAGGCTC 38
QY 1645 CAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAG 1681
Db 37 CAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAG 1

RESULT 7
CD636012/c
LOCUS CD636012 530 bp mRNA linear EST 12-JAN-2004
DEFINITION 56033904J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD636012
VERSION CD636012.1 GI:40284279
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 530)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
source
location/Qualifiers
1..530
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 18.9%; Score 517.4; DB 6; Length 530;
Best Local Similarity 99.6%; Pred. No. 6.5e-140;
Matches 529; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1151 AACTAATGATACAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAAATTCGCCATGCAAGC 1210
Db 530 AACTAATGATACAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAAATTCGCCATGCAAGC 471
QY 1211 CAGATCTGACAGTGAGCCGACATACAGCGGACCCATCTGCTGCGAGACCTCTCGACCA 1270
Db 470 CAGATCTGACAGTGAGCCGACATACAGCGGACCCATCTGCTGCGAGACCTCTCGACCA 411
QY 1271 AGAGGCTCATGACAGAGTCTCTCACTCTTTAAACCTTTGTGCGACATCAAAAGTGAAGTCC 1330
Db 410 AGAGGCTCATGACAGAGTCTCTCACTCTTTAAACCTTTGTGCGACATCAAAAGTGAAGTCC 351
QY 1331 AGAGTCTGTTCTGGTTTCCCTGGAGTGTCTGAGAGAGTGTAGTACACGCGCAAGATC 1390
Db 350 AGAGTCTGTTCTGGTTT-CCTGGAGTGTCTGAGAGAGTGTAGTACACGCGCAAGATC 292
QY 1391 ATTCCAGGACTTTTCCCATGGAAACCAACACAGCTTTAGTACAACTCCATCCCAAGATA 1450
Db 291 ATTCCAGGACTTTTCCCATGGAAACCAACACAGCTTTAGTACAACTCCCAAGATA 232
QY 1451 AAATGCCCTACATCCAAAATCTGTCACTACTCCCCCAAGGACAGAACTGAGGACAACTG 1510
Db 231 AAATGCCCTACATCCAAAATCTGTCACTACTCCCCCAAGGACAGAACTGAGGACAACTG 172
```



```
QY 1294 CTCTTTAACCCCTTTGTCGGAC-ATCAAGTGAAGTCCAGAGCTGTTCTCATGTGTTCCCT 1352
Db 1387 GACAAAATCCCAATGACCAACTCTCCAAATCTCGATCCACTGCGCCCAACCTGAAAATCAAA 1446
QY 1353 GCGAGTGTCTGAGAGAGCTGAGTACCAAGCAAGAAATCATTTCCAGGACTTTTCCCATGG 1412
Db 1447 GTGTACAAACACTCAGTGTCTGTCAACCCCAAGATGACCTCTCTGAGTTAGTCAAG 1506
QY 1413 AAACAACCAAGCTTTAGTACAATGATCCAGAAATAAAATGCCCTACATCCAAATCT 1472
Db 1507 CTGTCCCTCAGATGACCCAGTCTGTTGAGAAATGAAGCCCTCAGCCCTGAAGAACCAG 1566
QY 1473 GTCATCACTCCCAAGGACAGACT--CAGGACAACTGCTCTTTGGCCATTAGGG 1530
Db 1567 AGTCTAGCAAGGAGACTGATCTCCTGTACCGCATTTGGCAGCTTCAACTCGCTGGGA 1626
QY 1531 GCGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACACACGCGTGCATCCCA 1590
Db 1627 GGTCACTTATGTTCCCAATTCAGGAGTCAGCTTGTGTATCCCGTGGGCAATCC 1686
QY 1591 GAGGAGAAATTTGGGAGATTTATATGTCCATCAACCAAGGTGAACC---CAGCCTCCAG 1647
Db 1687 CAAGGGAGAGTCTACGAAATGTATGTACTGTATACAGGAAAGAAACTATGAGGCCACCC 1746
QY 1648 TCAGATGGCTCTGAGGTGCTCTGAGTCTCTGAAGTCACTGTGCTCTCCAGACATGATC 1707
Db 1747 ATGGATGACTCTCAGACACTTTTGAACCCCTGTGTGAGCTGTGGGCCCCAGAGCTCTG 1806
QY 1708 GTCAACCACTCCCTTTGCAATGACCATCCCGCACTGTGCAGATGTCTGAGCATTTG 1767
Db 1807 CTCACCGCCAGTGTCTCTCATATGATCACTTGCAGACCCCATATCCGAGGACTGG 1866
QY 1768 AATATCACTTTAAGAGAGGACACACAGCGGCAAAATGGAGGAAGTGTGTCAAGTGGAA 1827
Db 1867 AAAATCTGTCTCAAGAACGAGGACGACAGGAGAGTGTGGAGATGTGGTGTGGTGGG 1926
QY 1828 GATGAA-----TCTACATCCTGTACTGCTTTTGGACCCCTTTTGGAGCCCTTTGGTGTCAATGCTC 1881
Db 1927 GAGGAAAACTTCAACACCCCTCTGACTACATTCAGTGTGATGAGGAGGCTTGCACATCTC 1986
QY 1882 CTGCGACGCTTTGCGACCTATGCGCTCACTGGAGAGCCATACAGACTGTGCGGTGAAG 1941
Db 1987 ACAGAGAACTCAGCACTTACGCCCTGATAGGAACTTCCACCAACCAAGCGGTGCGAAG 2046
QY 1942 CAATGAAAGTGGCGGTTTTTGGCTGCATGCTCTGTAACCTCCCTGGATTACAATTTGAGA 2001
Db 2047 CGCCTCAAGCTGGCCATCTTTGGGCCCTCTGTCTGCTCTCTCGCTGGAGTACAGCATCCGA 2106
QY 2002 GTTTACTGTGTGACAAATACCCCTTGTGCAATTTTCAGGAAGTGGTTTCAGATGAAGGCAT 2061
Db 2107 GTCTACTGTCTGGATGACACCCAGGATGCCCTGAAGGAAATTTTACATCTTTGAGACAG 2166
QY 2062 CAAGGTGGACAGCTTCTGGAAGAACCAAAATGTGCAATTTCAAAGGAATACCTTTAGT 2121
Db 2167 ATGGAGGACAGCTCTTAGAAGAACTTAAAGCTCTTCATTTTAAAGCAGCACCCCAAC 2226
QY 2122 CTTTCAGATTTCTGTCTTGTATTTCCCCCAATTCCTCTGGAGAAATTAACCACTCACTGCC 2181
Db 2227 CTGCGCTGTCAATTCACGATATCGCCCATTCCTCTGGAAGAGCAAAATTTGCTGGCTAAA 2286
QY 2182 TGCAGGAAGTCCGCTTCTCCGCGTGTGTGCAATTAACCGGAGCCCTTGCATGTGCC 2241
Db 2287 TATCAGGAAATTCATTTTACCATGTTTGGAGTGGATCTCAAGAAACCTTGCACCTGCACC 2346
QY 2242 TTCTCCTGAGCGTTATAGCCCACTTACCACCCAGCTGCTTCCGAAATCTGCATTCGG 2301
Db 2347 TTCCTCTGGAAGATTTAGCCTGAACACAGTGGAGCTGTTTTCGAAACTCTTGTGTGGG 2406
QY 2302 CAGCTCAAGGCGCATGAACAGATCTCTCAAGTGCAGACATCAATCTCTAGAGAGTGAACGA 2361
Db 2407 CAGGTGAAGGAGAAAGGCGAGATCTTCCAGCTCACTGACCGTGTCTCAGAGGAACTTACT 2466
```

```
QY 2362 GAAACCATCACCTTTCTTCGCAAGAGGACAGCACTTTCCCTGTCACAGACTGSCCCCAAA 2421
Db 2467 GGCATCGATTGTCGCGCTGCTGGATCTCTGGAAACACCATCACCGTTCACGGGGCCAGT 2526
QY 2422 GCCTTCAAAATTCCTTACTTCCATCAGACAGCGGATTTGTGTACATTTGTATACCCCAAT 2481
Db 2527 GCTTTTCAGCATCCCTCTCTCCCTATTCGGCAGAAAGCTCTGTAGCAGCCTGGATGCCCCAG 2586
QY 2482 GCCAAAGGCAAGACTGGCAGATGTTAGCACAGAAACACAGCATCAACAGGAATTTATCT 2541
Db 2587 ACAGAGGCGCATGACTGGAGGATGCTGGCCCAATAGCTGAACCTGGACAGGTACTTTGAAT 2646
QY 2542 TATTTTCGTACACAAAGTAGCCCATCTGTGTCTCATTTTGAACCTGTGGGAAGCTCGTCAT 2601
Db 2647 TACTTTGCCACCAATATCCAGCCCACTGCGGTATATCTGTGATCTTTGGNAGCACAGAAC 2706
QY 2602 CAGCATGATGATGATCTTGACTCCCTGGCTGTGGCTTTGAAGAGATTTGGAGGACACAC 2661
Db 2707 TTCCACAGATGGAACCTGAGCATGCTGGCAGCTGTCTTGGNAGAAATGGAGACATGAA 2766
QY 2662 ACGAAACTCTCAACATTTTCAGAAATCCAGCTTGA 2696
Db 2767 ACGGTGTGTCTCTTAGCAGCAGAAAGGCGAGTATTA 2801

RESULT 9
AY411747 2532 bp DNA linear GSS 12-DEC-2003
LOCUS Homo sapiens HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY411747
VERSION AY411747.1 GI:39767715
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2532)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2532)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1..2532
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>2532
/locus_tag="HCM4327"
gene
ORIGIN
Query Match 18.0%; Score 491.6; DB 9; Length 2532;
Best Local Similarity 54.5%; Pred. No. 4.4e-132;
Matches 1380; Conservative 0; Mismatches 909; Indels 243; Gaps 10;
QY 326 TGAAGTCCGCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGC 385
Db 2 TCGGGGTGCGGAGGTGCAGATCAGGTGTCGGCGCAGGAGGTGGAGGAGCTCTTTGGCG 61
```

386 CCGAGGACTATTGGTGCAGTGTGTGGGTGGAGCCACCTGGGTACCTCTCAAGAGCAGGA 445  
Db  
62 TGGAGGATTTACTGTGTGCAGTGTGTGGGTGGAGCTCCGGGGCACCACCAAGAGTGC 121  
Qy  
446 AGGCTCTGTGGCATAGCTATTATCGGAAATTTGAACAGACCCACAGGAGGG 505  
Db  
122 GAGCTTACGTCCGATCGCTTACCTGCGAAGAACTTCGATCAGAGCCCTCTGGGCAAG 181  
Qy  
506 AAGTTCCTATTGAAGGCATGATTGTACTGTCACTGCCGCCACACAGAGGAGTCCCTGCTG 565  
Db  
182 AGTGGCCCTGGACCATAGGTTCTCTGTGAGTGGCCGCCCGCGAGGGGTGCTGTGG 241  
Qy  
566 CCGAGGTGAATGTGCTGAAATAAGAGGCCATTTGACTCTGAAACAGAGCAGAAATG 625  
Db  
242 CCGAGGTGAATGTGCTCAAGAAATGAGATGTCTATCGACCCACCCAGGACACCAACTTC 301  
Qy  
626 ACACCGGGCTGACCAATAACCTGATCATCAGGAGGACGAGCTCTGGACTCAGGAATT 685  
Db  
302 TGCTCACCATCGACCAACCTCATCATCCGAGGCCCGCCCTGTGGAACACTGCCAACT 361  
Qy  
686 ACACCTGCATGGCAGCCCAACATCGTGGCTAAGAGGAGAAAGCCTGTGGCCACTGTTGTGG 745  
Db  
362 ATACCTGCGTGGCCAGAAACATCGTGGCCAAACGCCGGAGCACCACCTGCCACCTCATCG 421  
Qy  
746 TCTACGTG----- 753  
Db  
422 TCTACGTGAATGGCGGTGCTCCAGCTGGGCAGAGTGGTCACCTGCTCCAAACCGCTGTG 481  
Qy  
754 ----- 753  
Db  
482 GCCAGGCTGGCAGAGCGCACCGGACCTGCACCAACCCCGTCCACTCAACGGAGGG 541  
Qy  
754 -----GATG 757  
Db  
542 CCTTCTGCGAGGCGCAGGCATTCCAGAAAGCCGCTGCACCACTGCGCCAGTCGATG 601  
Qy  
758 GGAGCTGGAAATGTGTGAGGAAATGTGTCCTGTGAGTCCAGAGTGTGAACATTGGCGGA 817  
Db  
602 GGGCGTGGACGGAGTGGAGCAAGTGTGTGAGCTGCAGCACTGAGTGTGCCCACTGGCGTA 661  
Qy  
818 TCCGGAGTGCACAGCACCAACCCCGAGAAATGGGGCAAAATTCGTGAAGTCTAAGCC 877  
Db  
662 GCGCGAGTGCATGGCGCCCAACCCAGAAACGGAGCCGTGACTGCAGCGGACCGTGC 721  
Qy  
878 AGGAATCTGAAACTGCACAGATGGTCTTTGCACTCTAGATAAAAAACCTCTTCATGAAA 937  
Db  
722 TCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAATAAGAAACTCTAAGCGACC 781  
Qy  
938 TAAACCCCAAGCATTGAGAAATGCCAGCAGCAATGCTTTGTACTCGGGCTTGGGTGCTG 997  
Db  
782 CCAACAGCCACCTGCTGGAGGCTTCAGGGGATGCGGCTGTATGCGGGGCTCGTGTGTG 841  
Qy  
998 CCGTGTGGCCGTTGCAG-----TCTGTGTCAATGGTGTACCCCTTACAGACGGAGCC 1051  
Db  
842 CCATCTTCGTGGTGTGGGCAATCCTCATGGCGGTGGGGGTGGTGTATCCGCGGCAACT 901  
Qy  
1052 AGAGTGACTATGGCTGGAGCTCAATTGAC---TCTTCTGCAATTGACAGGTGGCTTCAGAA 1108  
Db  
902 GCGGTGACTTCGACACAGACATCACTGACTCATCTGCTGCTGCTGACTGTGTGTTTCCACC 961  
Qy  
1109 CCTTCAACTTCAAAACAGTCCGTCAGCCGCAAGAAATATCATGGAACCTAATGATACAGAAA 1168  
Db  
962 CCGTCAACTTTAAGACGGCAAGCG----- 985  
Qy  
1169 AATCCTTTGTGTAATCTCCCTGCTCTGAAATTCCTGCCATGAGCCAGATCTGACAGTGA-- 1226  
Db  
986 -----CCAGCAACCGAGCTCCTACACCCCTCTGTGCTCTCTGACTCTGACAGCCAGCG 1039  
Qy  
1227 -CCGACATACAGCGGACCAATCTGT---CTGAGGACCCCTCTGGACAGAGGCTCATGA 1282  
Db  
1040 CCGGCATCTACCGCGACCGCTGTATGCCCTGCAGGACTCCACCGACAAATCCCACTGA 1099  
Qy  
1283 CAGAGTCTCTCTTTAACCCCTTTGTCGACATCAAGAGTGAAGTCCAGAGCTCGTTCA 1342

1100 CCAACTCTCTCTGCTGGACCCCTTACCAGCGCTTAAGGTCAAGGTCTACAGCTCCAGCA 1159  
Qy  
1343 -----TGGTTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAACGCAAGAAATCAITTC 1396  
Db  
1160 CACGGGCTCTGGGCGAGGCTTGGCAGATGGGGCTGACCTGTGGGGGTCTTCCCGCTG 1219  
Qy  
1397 GGAATTTTCCCATGGAACCAACACAGAGCTTTAGTACAATGATCCACAGAAATAAATATGC 1456  
Db  
1220 GCACATACCTAGCGATTTGCGCCGGGACACCACTTCTGTGACCTTCGCGAGCGCCAGCC 1279  
Qy  
1457 CCTACATCAAAATCTGTGCATCACTCCCAACAGGACAGAACTGAGGACAACTGGTGTCT 1516  
Db  
1280 TCGGTTCCAGCAGCTCTTTGGGCTGCCCCGAGACCCAGGAGCAGCGTCAGCGGACCT 1339  
Qy  
1517 TTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTGAGCTTACTCATACCAC 1576  
Db  
1340 TTGGCTGCTGGGTGGGAGGCTCAGCATCCCGGACAGGGGTGAGCTTGTCTGGTCCCA 1399  
Qy  
1577 ACGGTGCCATCCAGAGGAGAAATTTCTGGGAGATTTATATGTCCATCAACCAAGGTGAAC 1636  
Db  
1400 ATGGAGCCATTTCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAGGACAGAA 1459  
Qy  
1637 CAGGCTCCAG---TCAGATGGCTCTGAGGTGCTCTGAGTCTCTGAAGTCACTGTGGTC 1693  
Db  
1460 GTACCTCCCGCTTTTCAAGAGGACCCAGACAGTATTGAGCCCTCGGTGACCTGTGGAC 1519  
Qy  
1694 CTCACAGATATCGTCACCACTCCCTTTGCAATGACCACTCCGCACTGTGCAGATGTCA 1753  
Db  
1520 CACAGGCTCTCTGTGTGCGGCCCGTCACTCTACCAATGCCCCACTGTGCCAAGTCA 1579  
Qy  
1754 GTTCTGAGCAITTTGGAATATCCATTTAAAGAGAGGACACAGCAGGGCAAAATGGAGGAAG 1813  
Db  
1580 GTGCCGCTGACTGGAATCTTTAGCTCAAGACCCAGGCCCAACAGGGSCCACTGGAGAGG 1639  
Qy  
1814 TGAATGCTGAGTGAAGATGAATCT-----ACATCTGTGTACTGTCTTTTGGACCCCTTTG 1867  
Db  
1640 TGGTGACCTTGTGATGAGGAGACCTTGAAACACACCTGTACTGCCAGCTGGAGCCAGGG 1699  
Qy  
1868 CGTGTCAATGTCTCTGAGACAGCTTTGGGACCTATCGGCTCACTGAGAGACCAATCACAG 1927  
Db  
1700 CTTGTCAATCTGTCTGAGACAGCTGGGCACTTAAGTGTACGGGCGAGTCTATTTCCC 1759  
Qy  
1928 ACTGTCCGTGAGCAAACTGAAGGTGGCGTTTGGCTGCAATGCTGTAACTCCCTG 1987  
Db  
1760 GCTCAGAGCTCAAGGGCTCCAGTGGCGCTCTTGGCCCGCCCTCTGCACCTCCCTG 1819  
Qy  
1988 ATTACAACTTGAGATTTACTGTGTGGCAATACCCCTTGTGCAATTCAGGAAGTGGTTT 2047  
Db  
1820 AGTACAGCTCCGGGTCTACTGCTGGAGGACACGCTGTAGCACTGAAGGAGGTGCTG 1879  
Qy  
2048 CAGATGAAGGATCAAGGTGGACAGCTCTTGGAGAACCAAAATTCCTGCAATTTCAAAG 2107  
Db  
1880 AGCTGGAGCGGACTTGGGGCGGATCTTGGTGGAGGAGCGGAAACCGCTAATGTTCAAG 1939  
Qy  
2108 GGAATACCTTTAGTCTTCAGATTTCTGCTTTGATATCCCCCAATTCCTCTGGAGAAATTA 2167  
Db  
1940 ACAGTTACCAACCTTGGCGCTCTCCCTCCATGACCTCCCACTGCCCCATTTGGAGAGCA 1999  
Qy  
2168 AACCATTTACTGCTGCCAGGAGTCCGTTCTCCGGGTGTGGTGCAGTAACCGGAGC 2227  
Db  
2000 AGCTGTGGCCAAATACAGGAGATCCCTCTTATCAATTTGGAGTGGCAGCCAGAGG 2059  
Qy  
2228 CCTGTCACTGTCTCTTCCCTGGAGCGTTATAGCGCCACTACCAACCCAGCTGTCTCTGCA 2287  
Db  
2060 CCTTCACTGCACTTTCACTCTGGAGAGGCAAGTGTGGCTTCCACAGAGCTCACCTGCA 2119  
Qy  
2288 AAATCTGATTCGGAGCTCAAGAGCCATGAACAGATCTTCAAGTGCAGACATCAATCC 2347  
Db  
2120 AGATCTGCTGCGCAAGTGAAGGAGGAGGCGCAGATATTCAGGCTGCATACCACTCTG 2179  
Qy  
2348 TAGAGTGAACAGAGAAACCAT---CACTTTCTTCGACAAAGGAGCAGCATTTCCCTG 2404

Db 2180 CAGAGACACCTGTGGCTCCCTGGACACTCTCTGCTCTGCGCCCTGGCAGCACTGTACCA 2239

Qy 2405 CACAGACTGCCCAAGACCTTCAAAATTCCTTCACTCCATCAGACAGCGGATTTGGCTA 2464

Db 2240 CCCAGCTGGACCTTATGCTTCAAGATCCCACTGTCTCCATCCGCGCAGATATGCAACA 2299

Qy 2465 CATTGATACCCCAATGCCAAGGCAAGCACTGGCAGATGTTAGCAGAAAAACAGCA 2524

Db 2300 GCCTAGATGCCCCCACTCAGCGGCGCAATGACCTGGCGGATGTTAGCAGAAAGCTCTCTA 2359

Qy 2525 TCAACAGCAATTTATCTTATTTGCTACACAAAGTAGCCCATCTGCTGTCTATTTTGAACC 2584

Db 2360 TGCACCGGTACTGATTTATCTTGGCCACCAAGGAGCCCAACGGGTGTGATCTCTGGACC 2419

Qy 2585 TGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGTGATCCCTGGCCTGTCCTTTGAAG 2644

Db 2420 TCTGGGAAGCTCTGCAGCAGGACGATGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGG 2479

Qy 2645 AGATTGGGAGA 2656

Db 2480 AGATGGGCAAGA 2491

RESULT 10

AK031655

LOCUS

DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030473H24 product:unc5 homolog (C. elegans) 3, full insert sequence.

ACCESSION AK031655

VERSION AK031655.1 GI:26327502

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253

REFERENCE 2 Genome Res. 10 (10), 1617-1630 (2000) 10349636

REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Onedaka, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913

REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 11076861

REFERENCE 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

## JOURNAL REFERENCE

Nature 420, 563-573 (2002)

6 (bases 1 to 3790)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuto, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

## Direct Submission

## TITLE JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

## FEATURES

## source

1. 3790

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="FANTOM DB:6030473H24"

/db\_xref="taxon:10090"

/clone="6030473H24"

/sex="male"

/tissue type="testis"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="13 days embryo"

118..2970

## CDS

/note="unnamed protein product; putative

unc5 homolog (C. elegans) 3 (MGD|GI:1095412,

GB|NM\_009472, evidence: BLASTN, 99%, match=464)"

/codon\_start=1

/protein\_id="BAC27495.1"

/db\_xref="GI:26327503"

/translation="MRKGLRATARCGLIGYLLQMLVLPALALLSASGTGSAQDDE  
FHELPETFPDPEPLPHLEPEAYIVKKNVLYCKASPATQIYFKCNSEWHQ  
KOHVDERVDETSGLIVREVSIEISQVBEELFGPDYWCQCVAMSGAGTTKSKAYV  
RIAYLRKTEOPLGKESLQEVLLQCRPEGI PVAEVELKNEIDIDAEENFYI  
TIDNLLIQARLSDPANTCVAKIVAKKSTATVIVVNGMTWTSVCSNRC  
GRRQKRTCTNPAPNGAFCEGSGVQKIACITLCPVDGRTWSKWSKTCGTECH  
WRRCTEAPAKNGKCDGLVKNCKTGLCMQCFIYPDTEHRPQNSYGFSSAD  
SDDLAVPLDTSAAMYPGPVLDHVSQDKIPMTNSPILDPILNLIKVNSSGAVT  
RQDGLVPLDTSAAMYPGPVLDHVSQDKIPMTNSPILDPILNLIKVNSSGAVT  
PQDLAEFSKLSQSLLENEALNKQSLAROTDPSCTAFGTGNSLGGHLIIPN  
SGVSLIPAGAIPOGRVEMYTVHKKNNRPWEDSOTLLTPVSGCGPGLLTRPV  
ILFLHHCADPSTEDWKIQKNQAVQWQEDVVVVGGENFTTPCYIQLDABACHLTEN  
LSTYALVQSGSTTKAAARLKLAIPLCCSSLEYSIRVCLDDTDQALKEVLQERQM  
GGQLEEKALRFKGIHNLRIHDIHSLKSLKLAQOEIPFYHWSGQRNLHC  
TPTLERLSINTVELVKLCVROVEGEGQIFQLNCTVSEEPDGLDPLDPASTITVT  
GPSAFSIPLPKLCSSLDAPOTRGHDWRMLAKNLNLDRLVNFATKSSPTGVILDL  
WEAQNPFDGNLSMLAAVLEBEMGRHEITVYLAESQY"

## ORIGIN

Query Match 17.4%; Score 476.4; DB 3; Length 3790;  
Best Local Similarity 52.6%; Pred. No. 1.5e-127;  
Matches 1419; Conservative 0; Mismatches 1146; Indels 135; Gaps 12;

Qy 90 CGCGGTGCCCCGAGGAACACTGACATGCGGAGCCCTTCCGGAATCCATCCATCCATCAG---C 146







QY 1086 TGCAATTCAGAGTGGCTTCCAGACCTTCAACTTCAAACAGTCCGTCAGCCCAAGAAATAT 1145  
 Db 1120 TGATGTGGCTCTCTAAGTGGGATGATGATCGCTGTAAAGTGTGTCTGGCGATCACTGT 1179  
 QY 1146 CATGG-----AACTAATGATACAGAAATCCCTTTGGTAACCTCCCTGCT 1190  
 Db 1180 TGTGGTGGCCCTGTTTGTGTATCGGAAGAACACCGTGAATTTGAGTCTGACATATTGA 1239  
 QY 1191 CTTGAATTTGCGCATGACGCCAGATCTGACAGTGGCGGACATACAGCGGACCCATCTG 1250  
 Db 1240 CTCCTCAGCACTCAATGGCGGCTTTTCAGCGTGTGAACATCAAGGCTGCCAGACAAGATCT 1299  
 QY 1251 TCTGCGAGACCTCTGAC-----AAGGAGCTCATGACAGAGTCTCACT 1295  
 Db 1300 CTTGGTGTCTCCCTGACCTCACTCAGCTGAGCGGATGATGACAGGACCTGTCTATGC 1359  
 QY 1296 CTTTAAACCTTTTGGGACATCAAGTGAAGTCCAGAGCTGCTTATGATGTTTCCCTGGG 1355  
 Db 1360 TCTGATGATGTCTCAGACAAATCCCAATGACCAACTCTCCAATTTCTGGACCACTAGC 1419  
 QY 1356 AGTGTCTGAGAGCTGAGTACACCGCAAGAAATCAATCCAGGACTTTCCAGGACTTT----- 1403  
 Db 1420 CAACCTTGAAATCAAAAGTGTACACAGCTCAGGTGTCTCACTCTCAGGATGACCTTGC 1479  
 QY 1404 ----TCCCCATGGAACAACACAGCTTTTAGTACAATGCAATCCAGAAATATAAATGCCCT 1459  
 Db 1480 CGAGTCTCATCCAACTGTCAACCCAGATGACCCAGTCTCTGCTAGAGATGAGGCCCT 1539  
 QY 1460 ACATCCAAA-----ATCTGTCTCATCTCCCAACAGGACAGAACTGAGGACAACTGGTGT 1514  
 Db 1540 TAACTTGAAGAACAGAGCTCGCAAGACAGACTGACCCATCTCGACAGCAATTTGTATC 1599  
 QY 1515 CTTTGGCCATTTAGGGGGCTTAGTAATGCCAATACAGGGGTGAGCTTACTCATACC 1574  
 Db 1600 CTTCAACTCTCTTGGGGGTCACTCATCTTCTTAATTCAGGAGTAACTGTCTGATTC 1659  
 QY 1575 ACAGGTGCCATCCACAGAGAGATTTCTGGGAGATTTATATGTGCCATCAAC-----AAGG 1631  
 Db 1660 CGCTGGGGCCATTCCTCAGGGGAGTCTATGAATGTATGTGACTGTACACAGGAAGA 1719  
 QY 1632 TGAACCCAGCTTCAGTCAAGTGGCTCTGAGGTGCTCTGAGTCTGTAAGTCACTGTTGG 1691  
 Db 1720 AAATATGAGGCCCCCACTGGAAGACTCTCAGACCTTACCCCTGTGTGAGCTGTGG 1779  
 QY 1692 TCCTCCAGACATGATCTGCACCTCTCCCTTGCATTCACCATCCGCACTGTGCAGATGT 1751  
 Db 1780 GCCTCTGAGCTCTGCTGACCCCTCTGTCTCTCTGATCTCTGATCTGATCTGTGAGACCC 1839  
 QY 1752 CAGTTCTGAGCATTTGAATATCCATTTAAAGAGAGGACACAGCAGGGCAAAATGGGAGGA 1811  
 Db 1840 CAGCACCGAGACTGGAAGATCCAGCTCAAAACCCAGGACGTGAGGACAAATGGGAGGA 1899  
 QY 1812 AGTGATGTGAGTGAAGATGAT-----CTACATCTCTGTACTGCTTTTGGACCCCTT 1865  
 Db 1900 TGTGTGTGTGTGGGAGGAGAACTTTCAACACCCCTGTGTATTCAGTGTGATGAGGA 1959  
 QY 1866 TGGCTGTCTGCTCTGAGACCTTTGGGACCTATGCGCTCACTGGAGAGCAATCAAC 1925  
 Db 1960 GGCTTGGCATATCTTCAGAGAACCTCAGTACCTATGCGCTGTGTGGCAGTCCACCAC 2019  
 QY 1926 AGACTGTGCCGTGAAGCACTGAAGGTGGCGGTTTTTGGCTGCAATGCTGTAACTCCCT 1985  
 Db 2020 CAAAGCAGCTGCCAAGGCTTTAACTGGCCATCTTTGGGCCCTCTGCTGCTCTCCCT 2079  
 QY 1986 GGATTACACTGTAGATTTACTGTGTGGAATAACCCCTGTGCTATTCAGGAGGAGTGT 2045  
 Db 2080 GGAGTACAGCAATGAGTCTACTGCTGGATGACACAGAGATGCCCTCGAGGAGTGTCT 2139  
 QY 2046 TTCAGATGAAGGATCAAGGTGACAGCTCTCTGGAAGAACCAAAATTTGCTGCAATTTCAA 2105  
 Db 2140 ACACTGAGAGGCAATGGGAGGACAGCTCTTAGAGAACCCCAAGGCTCTTCAATTTAA 2199

QY 2106 AGGGAATACCTTTAGTCTTTCAGATTTCTGCTCTTGATATCCCCCAATTCCTCTTGAGAAAT 2165  
 Db 2200 AGGCAGCATCCACAACTGCGCTGTCTATTCAAGACATCGCCCAATTCCTCTTGGAAGAG 2259  
 QY 2166 TAAACCATTTCACTGCTCCAGAGAGTCCCGTCTTCCCGCGTGTGGTGCAGTAACCGGCA 2225  
 Db 2260 CAAATTTGCTGGCTAAGTATCAGGAAATTTCCATTTTACCACATCTGGAGTGGCTCTCAAAG 2319  
 QY 2226 GCCCTGCTGCTGCTCTCTCCCTGGAGCTTTATACGCGCCACTACCAACCCAGCTGTCTCTG 2285  
 Db 2320 AAACCTCTCACTGACCTTCACTCTGGAAGACTCAGCCTAAACACAGTGAAGTGGTTG 2379  
 QY 2286 CAAATATTCGCAATTCGGAGCTCAAAAGCCATGAACAGATCTCTCAAGTGCAGACATCAAT 2345  
 Db 2380 CAAACTCTGTGTGCGGAGGTGAAGGAGAGGCGAGATCTTCCAGCTCAACTGTACTGT 2439  
 QY 2346 CCTAGAGAGTGAACAGAAACCATCACTTTCTTCGCAAGAGGACAGCACTTCCCTGTC 2405  
 Db 2440 GTACAGAGAACCTACTTGGCATCGATTACTCTCTCTGGACCTGTAGTACCATCACCAC 2499  
 QY 2406 ACAGACTGGCCCCAAAGCCTTCAAAATTTCCCTACTTCCATCAGACAGCGGATTTGTCTAC 2465  
 Db 2500 TGTACCGGACCAAGTCTTTCAGCATCTCTCTCTATCCGCGCAGAACTATGCGACAG 2559  
 QY 2466 ATTGATACCCCAATGCAAGGCAAGGACAGTGGCAGATGTTAGCACAGAAAAACAGCAT 2525  
 Db 2560 CTTGATGCTCCCTCAACCAAGAGGCGCATGCTGGAGGATGCTGGGCCCAATAAACTCAACT 2619  
 QY 2526 CAACAGGATTTATCTTTTTCGCTACACAAAGTAGCCCATCTGCTGTCTATTGAACT 2585  
 Db 2620 GGACAGGATCTTGAATTTCTTCCACCAATTCGAGCCCACTGGGTAATCTCTGATCT 2679  
 QY 2586 GTGGGAGCTCTGCTATCAGCATGATGCTGATCTTCACTCCCTGGCTGTGCTGCTGAAAGA 2645  
 Db 2680 TTGGGAGGACAGAACTTCCAGATGGAACCTCTGAGCATGCTGGCAGCGCTCTGGAAGA 2739  
 QY 2646 GATTTGGAGGACACACAGAACTCTCAACATTTTCAGAAATCCCAAG 2691  
 Db 2740 AATGGAGACATGACAGATGCTGTCTTGGCAGCAGAGGACAG 2785

RESULT 12

AY411749 2532 bp DNA linear GSS 12-DEC-2003  
 Mus musculus HMC4327 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 LOCUS AY411749  
 DEFINITION AY411749.1 GI:39767717  
 ACCESSION GSS.  
 VERSION Mus musculus (house mouse)  
 KEYWORDS Mus musculus  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 2532)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 2532)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 FEATURES Location/Qualifiers

```
source      1..2532
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            <1..2532
            /locus_tag="HCM4327"

ORIGIN
Query Match      17.2%; Score 471.8; DB 9; Length 2532;
Best Local Similarity 54.0%; Pred. No. 2.9e-126;
Matches 1368; Conservative 0; Mismatches 922; Indels 243; Gaps 10;

Qy 325 TTGAAGTCCGCGAAGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGG 384
Db 1 TTGCGGTGCGAGAGTGCAGATGAGGTGTACGCGAGCAAGTGGAGGAATCTTTCGGG 60
Qy 385 CCGAGGACTATTGGTCCAGTGTGTGGCGTGGAGCCACCTCTGGGTACTCCAGAGCAGG 444
Db 61 CTCGAGGACTACTGGTCCAGTGGTGGCTGGAGCTCTTCGGGAATCTACAGAGTCCG 120
Qy 445 AAGGCTCTGTGGCATAGCTATTATACGGAAAACTTTGAAACAAGACCACAAAGGAAG 504
Db 121 CGAGCTTACATCCGCAATGGCTACTTTCGCAAGAACTTTGACCAAGAGCCTCTGGCCAAG 180
Qy 505 GAAGTTCCTCCATTGAAGCATGATTGTACTGCATCTGCCGCCACACAGAGGAGTCCCTGCT 564
Db 181 GAGTACCTTTGATCATATGAGGTCTTCTGAGTGGCGCCACCGGAGGAGTGCCTGTG 240
Qy 565 GCGAGGTGAAATGGCTGAAATGAAAGAGCCCAATTGACTCTGAACAAGACGAGAACATT 624
Db 241 GCTGAGTGGAAATGGCTCAGAAATGAAGATGTCTATGACCCCGCTCAGGACACTTACTTC 300
Qy 625 GACACAGGCTGACCAATACCTGATCATCAGGACGACCGCTCTCGGACTCAGGAAT 684
Db 301 CTGCTACCAATGACCAACACCTCATCATCGCCAGCGCGCTCTCAGACACGCGCAAC 360
Qy 685 TACACTGCTAGCAGCCACATCGTGGCTTAAGAGAGAGCCCTGTGGCCACTTGTGTG 744
Db 361 TACACTGTGTGGCAGAAATATATGTGGCCAAAGCGCCGAGCACACCGGCCACAGTCA 420
Qy 745 GTCTACTGTGATGGAGC----- 762
Db 421 GTCTATGTGAATGGAGCTGGTCCAGCTGGGCGAGAGTGGTCAACCTGTTCCAATCGCTGT 480
Qy 763 ----- 762
Db 481 GGCGAGGCTGCGAAGAGCGTACTCGGACCTGCACCAATCCAGCCCACTCAATGGAGGC 540
Qy 763 ----- 762
Db 541 GCCTTCTGTGAGGACAGGCTTCCAGAAACAGCTTGGCAACCGGTGTGCCAGTGGAT 600
Qy 763 -----TGGGAAGTGTGGAGCGAATGTGTGGTCTGCAAGTGTGAACATTTGCGG 816
Db 601 GGAGCGTGGACCGAGTGGAGCAAGTGTGTGCTGCAAGCAAGAGTGTGCGACTGGCGC 660
Qy 817 ATCCGGAGTGCACAGCACCAACCCCGAGAAATGGGGGCAAAATTCGTGAAGGTCTAAGC 876
Db 661 AGCGCGAGTGCATGGCACCGCCACCCAGAACCGAGGCGGTGACTGCAGCGGAGCGCTA 720
Qy 877 CAGGAATCTGAAACTGCACAGATGGTCTTTGCAATCTAGATAAAACCTCTTCATGAA 936
Db 721 CTTGACTCCAGAACTGCACTGTATGGGCTGTGGTGTGCTGAATCAGAGAACTCTTAAACGAC 780
Qy 937 ATAAACCCCAAAGCATTTGAGATGCGCAGCGACATTTCTTTGTACTCGGCTTGGGTGCT 996
Db 781 CCTTAAAGCCACCCCTGGAGACATCGGAGATGTGGCACTGTACGAGGCTTGTGGTG 840
Qy 997 GCGGTGTGGCGGTGTGAG-----TCTTGTGCTATTGGTGTCACTCCCTTTACAGACGAGC 1050
Db 841 GCCGTCTTTGTGGTGTGAGCGGTCTCATGCGCGTGGAGTGTGCTATACCGGAGAAAC 900
Qy 1051 CAGAGTACTATGGCGTGGAGCGTCAATTGACTCTTCTCT---GCATTGACAGGTGGCTCCAG 1107
```

```
Db 901 TCGCGGACTTTCGACACGGACATCACCGACTCTCTCGCGCCCTCCTCTGGTGGCTTCCAC 960
Qy 1108 ACCTTCAACTTCAAAAACAGTCCGTCAGCAAGCAAGAATATCATGGAACATAATGATACAAGAA 1167
Db 961 CCTGTCAACTTCAAGACTGCAAGGCCAAC----- 990
Qy 1168 AATATCCTTTGGTAACTCCCTGCTCTGAAATTTGCGCAATGCGACGACAGATCTGACAGTGA- 1226
Db 991 -----AACCGCAGACTCCTGCAACCGTCCGCCCCCTCCAGACCTTAACCGCCAGT 1038
Qy 1227 --CGGACATACAGCGGACCCCATCTGT---CTCAGGACCTCTGGAACAAGGAGCTCATG 1281
Db 1039 GCTGGCATCTACCGCGGCTGTGTATGCGCTCGAGGACTCCGCGCAAGATATCCCATG 1098
Qy 1282 ACAGAGTCTCTACTCTTTAAACCTTTTTCGGACATCAAAAGTGAAGTCCAGAGCTCGTTC 1341
Db 1099 ACTAAATTCGCCCTCTGTGGATCCCTGCCAGCTCAAGATCAAGTCTTATACTCCAGC 1158
Qy 1342 ATGGT-----TTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAACGCAAGAAATCATTC 1395
Db 1159 ACCATCGTGTCTGGGTCTGGCTGTGATGGAGCCGACCTGTCTGGGTGTCTCTCCGCCG 1218
Qy 1396 AGGACTTTTCCCATGSAACAACACAGCTTTAGTACATGATCATCCAGAAATAAAATG 1455
Db 1219 GGCAGGTACCCAGGCGAATTTCTCCGGGACACCCATTTCTGCACTTGGCGAGTGCAGC 1278
Qy 1456 CCCTACATCCAAAATCTGTCTCATCACTCCCAAGGACAGAACTGAGGACAACTGGTGT 1515
Db 1279 CTTGGTTCCAGACACCTCTCTGGGCTTACCTCGGACCCAGAGAGCTGTGACGGCACC 1338
Qy 1516 TTTGGCCATTTAGGGGGGCGCTTAGTAAATGCCAAAATACAGGGGTGAGCTTACTCATACCA 1575
Db 1339 TTTGGTTGGCTGGGAGGAGGCTGAGCTCCCGGACACAGGGGTGAGCTTGTGGTACCA 1398
Qy 1576 CAGGTGGCATCCAGAGGAGAAATCTTGGGAGATTTATATGTCCATCAACCAAGGTGAA 1635
Db 1399 AATGGAGCCATTTCCAGGGAAGTCTATGACCTGTATCATATCAACAAGGCCGAA 1458
Qy 1636 CCCAGGCTTCA---GTCCAGATGGCTCTGAGGTGCTCTGAGTCTCTGAAGTCACTGTGGT 1692
Db 1459 AGCACTCTCCACTTTCCAGAGGTTCCAGACAGTATTGAGCCCTCGGTGACCTGTGGG 1518
Qy 1693 CTTCCAGACATGATGTCACCACTCCCTTTGGCAATGACCAATCCCGCACTGTGCAAGATGTC 1752
Db 1519 CCCACAGGCTACTCTCTGCGCCCTGTCTGCTCAACCGTGGCCCACTGTGCTGAAGTCT 1578
Qy 1753 AGTTCTGAGCATTTGGAAATATCCATTTAAAGAGGACACAGAGGCAATGGAGAGAA 1812
Db 1579 ATCGCTGGAGACTGGATCTTTTTCAGCTCAAGCCAGGCCCATCAGGGCCACTGGGAGGAG 1638
Qy 1813 GTGATGTGAGTGAAGATGAATCT-----ACATCTGTTTACTGCTCTTTTGGACCCCTTT 1866
Db 1639 GTGTTGACCTTGAATGAGGAGACCTTCAACACACCTGCTACTGCTCCAGCTGGAGGCTAAG 1698
Qy 1867 GCGTGTCAATGTCTCTCGACAGCTTTGGGACCTATGCGGTCTACTGAGAGGCCAATCACA 1926
Db 1699 TCTGCGCACATCTCTGTGGACAGCTGGGTACCTACGTATTATTTGGCGAGTCTCTACTCT 1758
Qy 1927 GACTGTGCGGTGAAGCAATGAAAGTGGCGTGTGCTGCTGATGCTCTGTAATCCCTG 1986
Db 1759 CGCTCTGCACTGAAGCGGCTCCAGCTGGCCATCTTGGCCCCAGCCCTCTGCACCTCCCTG 1818
Qy 1987 GATTACAACTTGAGAGTTTACTGTGTGGCAATATACCCCTTGTGCTTTTCAAGGAGTGGTT 2046
Db 1819 GAGTATAGCTCAGGCTTACTGTCTGGAGGACACACTGTAGCATGAGAGGAGTCTCTG 1878
Qy 2047 TCAGATGAAGGCAATCAAGGTGACAGCTCTCTGGAGAAACAAATAATGCTGCAATTTCAA 2106
Db 1879 GAGCTGGAGAGGACTCTGGGTGGCTACTTGGTGGAGGAGCCCAAGCCCTTGTCTTTAAG 1938
Qy 2107 GGAATACCTTTAGTCTTTCAGATTTCTGCTCTTGTATATTCCTCCCATTTCTCTGGAGAT 2166
```



```
QY 1384 AAGAAATCATTCAGGACTTTTCCCATGGAAACACACAGCTTTAGTACATGATCC 1443
Db 60 AAGAACCATTCGGGACTTTTCCCATGGAAACATCACAGCTTTACGACAGTGCATCC 1

RESULT 14
AY411748
LOCUS 2532 bp DNA linear GSS 12-DEC-2003
DEFINITION Pan troglodytes HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY411748
VERSION AY411748.1 GI:39767716
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metazoa; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 2532)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2532)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1..2532
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..2532
/locus_tag="HCM4327"
gene
ORIGIN
Query Match 15.9%; Score 434.2; DB 9; Length 2532;
Best Local Similarity 53.8%; Pred. No. 3.3e-115;
Matches 1042; Conservative 0; Mismatches 821; Indels 75; Gaps 9;
QY 752 TGATGGAGCTGGGAAGTGTGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATT 811
Db 596 TCGATGGGCGTGGACGAGTGGAGCAAGTGGTCAAGCTGAGTGTGCCACT 655
QY 812 TGGGATCCGGAGTGCACAGCACACCCCGGAGAAATGGGCAAAATTTCTGGAAGTTC 871
Db 656 GGCCTGACCCGAGTGTGATGGCGCCCGCCACCCAGAACGAGGCGGTGACTGCAGCGGGA 715
QY 872 TAAGCAGGAAATCTGAAATCTGACACAGATGGTCTTTGCATCTTAGATAAAAACTCTTC 931
Db 716 CGTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCAATGCAAAATAGAAACTCTAA 775
QY 932 ATGAAATAAAACCCCAAGCATTGAGAAATGCCAGCGACATTGTTGTACTCGGGCTGG 991
Db 776 GCGACCCCAACAGCACCTCTGTGAGGCTTCAGGGATGGGCGCTGTATGGCGGGCTCG 835
QY 992 GTGTCGCGTGGTGGCGGTGGAG-----TCTGGTCATTGGTGTACCCCTTACAGAC 1045
Db 836 TGGTGGCGGTCTTCTNTGGTCTNTGGCAATCTCATGGCGGTGGGGGTGGTGTACCGCC 895
QY 1046 GGAGCAGAGTGTACTATGGCGGTGGACGTCATTGAC---TCTTCTGCAATTCACAGGTGGCT 1102
Db 896 GCAACTGCCGTGACTTCGACACAGACATCACTGACTCACTGCTGCGCTGACTGGTGGTT 955
```

```
QY 1103 TCCAGAGCTTCAACTTCAAAACAGTCCGTCAAGCCAAAGATATATCATGGAATCAATGATAC 1162
Db 956 TCCACCCCGTCAACTTAAAGACGGCAAGC----- 985
QY 1163 AAGAAAAATCTCTTTGGTAAATCTCCCTGCTCTGAATTTCTGCCATGTCAGCAGAGATCTGACAG 1222
Db 986 -----CCAGCAACCCGCGAGCTCTTACACCCCTCTGTGCTCTCTGACTGACAG 1033
QY 1223 TGAG---CCGGACATACAGCGGACCCATCTGT---CTGCAAGGACCTCTTGGAACAAGAGC 1276
Db 1034 CCAGCGCGGCATCTACCGCGGACCCGCTGTATGCCCTCGAGGACTCCACCGCAAAATCC 1093
QY 1277 TCATGACAGAGTCTCACTCTTTAAACCTTTTGGCAGCATCAAGTGAAGTCCAGAGCT 1336
Db 1094 CCATGACCAACTCTCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCT 1153
QY 1337 CGTTCA-----TGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTAGTACCAAGCAAGAATC 1390
Db 1154 CCAGCACTACGGGCTCTGGGCGAGGCTGGCAGATGGGCTGACCTGCTGGGAGTCTTGC 1213
QY 1391 ATTCAGGAGCTTTTCCCATGGAAAACAACACAGCTTTTAGTACAATGCAATCCAGAAATA 1450
Db 1214 CGCTTGGCACATACCTTAGCGATTTCCGCCGGGACACCACTTCTCTGCACCTCGCAGCG 1273
QY 1451 AATGCCCTACATCCAAATCTGTATCATCTCCCAAGGACAGAACTGAGGACAACTG 1510
Db 1274 CCAGCCTCGGTTCCCGAGCAGCTCTTGGGCTGCGCCGAGACCCAGNAGCAGCGTCAGCG 1333
QY 1511 GTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCAAAATACAGGGGTGAGCTTACTCA 1570
Db 1334 GCACCTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGTCAGCTTCTGCG 1393
QY 1571 TACCACACGCTGCCATCCAGAGGAGAAATCTTTGGAGATTTATATGTCCATCAACCAAG 1630
Db 1394 TGCCCAATGGAGCAATTCGCCAGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGG 1453
QY 1631 GTGAACCCAGCTCCAG---TCAGATGGCTCTGAGGTGCTCTGAGTCTCTGAAGTCACT 1687
Db 1454 CAGAAAGTAGTACCTTCCCGCTTTTCAAGAGGACCCAGACAGATGATTGAGCCCTCAGTGACCT 1513
QY 1688 GTGGTCTCCAGACATGATGCTCACCCTCTTGTGATTTGACATCCCGCCTCAGCTGTGCAG 1747
Db 1514 GTGGACCCACAGGCTCTCTGTGTGCAACCCCTCATCTCCACATGCCCCACTGTGCGG 1573
QY 1748 ATGTCAAGTTCTGAGCAATGGAATATCCATTTTAAAGAAGGACACAGCAGGGGCAAAATGGG 1807
Db 1574 AAGTCAAGTCCCGTGAATGATCTTTTCAAGTCAAGACCCAGGCGCCACAGGCGCACTGGG 1633
QY 1808 AGGAAGTGTATGTCAGTGGGAAGATGAATC-----TACATCTCTGTTACTGCTTTTGACC 1861
Db 1634 AGGAGGTGTGACCCCTGGATGAGGAGACCCCTGAACACACCCCTCTACTGCGAGCTGGAGC 1693
QY 1862 CTTTTCGCTGTATGCTGCTCTGACAGCTTTTGGGACCTATATGCGCTCACTGAGAGAGCAA 1921
Db 1694 CAGGGCTGTACATCTCTGCTGGACAGCTGGGCACTTACGTGTTTCACGGGCGAGTCTCT 1753
QY 1922 TCACAGACTGTGCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCAATGCTCTGTAACT 1981
Db 1754 ATTCCNNNNNNNCCGTCNNNNNGCTCCNGCTGGCGCTCTTNGCCCTCTGCGCTCTGCACT 1813
QY 1982 CCGTGAATTACAACCTTGAGAGTTTACTGTGTGACAAATACCCCTTGTGCAATTTTCAGGAAG 2041
Db 1814 CCGTGGANNNNNGCTCCCGGCTCTACTGCTGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGAGG 1873
QY 2042 TGGTTTTCAGATGAAGGCACTCAAGGTGGAGCAGCTCTCTGGAAGAACCAAAATATGCTGCAAT 2101
Db 1874 TGTGTGAGCTGGAGCGGACTCTGGGCGGATATCTTGTGTGAGGAGCGGAAACCCGTAATGT 1933
QY 2102 TCAAGGGAATACCTTTTAGTCTTTCAGATTTCTGTCTTGTATATTTCCGCCCAATCTCTCTGGA 2161
Db 1934 TCAAGGACAGTTTACCACAACTCGGCTCTCTCCCTCCATGATGACCTCCCCCAATGCGCATTTGA 1993
QY 2162 GAATTAAACCATTCACCTGCGCTGCGAGAGTCCGCTTCTCCCGGCTGTGTGTCAGTAACC 2221
```

```

Db 1994 GGAGCAGCTCTGCTGCCAAATACAGAGAGATCCCTCTTGTGCATTTGGAGTGGCAGCC 2053
Qy 2222 GGCAGCCCTGCACTGTGCTCTTCCCTCTGGAGCGTTATACGCCCACTACCAACCCAGCTGT 2281
Db 2054 AGAAGGCCCTCCACTGCACTTTACCCCTGGAGAGCAGAGCTTGGCTTCCACAGAGTCA 2113
Qy 2282 CCTGCAAAATGCAATTCGGCAGCTCAAGGCCATGAACAGATCCTCCAAAGTGAGACAT 2341
Db 2114 CCTGCAAGATCTGGTGGCGCAAGTGAAGGGGAGGCGCAGATATCCAGCTGCATACCA 2173
Qy 2342 CAATCTAGAGAGTGAACGAGAAACCAT---CACTTTCTTGGACAGAGGACAGCACTT 2398
Db 2174 CTCTGGAGAGACACCTGTGCTGCTTCCCTTGGACATCTCTGTCTGCCCCCTGGCAGCACTG 2233
Qy 2399 TCCCTGCAAGACTGGGCCCAAGCCCTTCAAAATTCCTACTCTCCATCAGACAGCGGATTT 2458
Db 2234 TCACCACCCAGCTGGGACCTTATGCTTCAAGATCCCACTGTCCATCCGCCAGAGATAT 2293
Qy 2459 GTGCTACATTTGATACCCCAATGCCAAAGCAAGGACTGGCAGATTTAGCAGAGAAA 2518
Db 2294 GCAACAGCCTAGATGCCCCCAACTCACGGGCAATGACTGGCGGATTTAGCAGAGAAC 2353
Qy 2519 ACAGCATCAACAGGAATTTATCTTTTTCGCTACACAAAGTAGCCCATCTGCTGCAATTT 2578
Db 2354 TCTCTATGGACCGTACTGATTTTGTGCTTGGCCAAAGGAGCGCCACCGGGTGTGATCC 2413
Qy 2579 TGAACTGTGGAGAGCTCGTCATCAGCATGATGTTGATCTTTGACTCCCTGGCCTGTGCC 2638
Db 2414 TGGACCTCTGGAGAGCTCTGCAGCAGCAGCATGGGACCTCAACAGCTTGGCGAGTCC 2473
Qy 2639 TTGAGAGATTTGGGAGGA 2656
Db 2474 TGGAGGAGATGGGCAAGA 2491

```

## RESULT 15

```

BU447189
LOCUS 603214135F1 CSEQRBN13 Gallus gallus cdna clone CHEST198e9 5', mRNA
DEFINITION sequence.
ACCESSION BU447189
VERSION BU447189.1 GI:25936500
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

```

```

REFERENCE
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken CDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .896
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST198e9"
/sex="Female"
/dev_stage="adult"

```

## FEATURES

```

source
Location/Qualifiers
1. .896

```

```

Search completed: April 1, 2005, 02:01:06
Job time : 8603 secs

```

```

/lab_host="DH10B"
/clone_lib="CSEQRBN13"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones: cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

```

## ORIGIN

```

Query Match 14.1%; Score 386.2; DB 5; Length 896;
Best Local Similarity 82.0%; Pred. No. 2.8e-101;
Matches 445; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
Qy 2194 CGTTTCTCCCGTGTGGTGCAGTAAACCGGCGCCCTGCACCTGCTTCTCCCTGGAG 2253
Db 2 CCATTCTCCCGTGTGGTGCAGTAAACCGGCGCCCTGCACCTGCTTCTCCCTGGAG 61
Qy 2254 CGTTATACGCCCACTACCAACCCAGCTGTCTCTGCAAAATCTGCAATTCGGCAGCTCAAAAGC 2313
Db 62 CGTTACACCCCTGCAACCAACACAGCTGTCTGCAAGATCTGGTCCGCAAGTCAAGGG 121
Qy 2314 CATGAACAGATCTTCAAAGTGCAGATCAATCTTAGAGATGAAGAGAACCATCAT 2373
Db 122 CAGCAGCAGATCCTAAGATCCAGATCCATCTCTCGAATGAAGAGAACCATTTGCT 181
Qy 2374 TTCTTCGCAAGAGGACAGCACTTTTCCCTGCAACAGCTGGCCCAAGCCTTCAAAAT 2433
Db 182 TTCTTCGCAACAGTACAGCAACTTCCCTGCAACAGTGGTGGCAAAAGCATTTCAAAATC 241
Qy 2434 CCTACTCCATCAGACAGCGGATTTGTGTACATTTGTATACCCCAATGCCAAAGGCAAG 2493
Db 242 CCATATTCCATCAGACAAAGAAATTCGCGGACGTTCCGACACACCAACCAATGCCAAAGGCAAA 301
Qy 2494 GACTGCGCATGTTAGCAGAGAAACAGCATCAACAGGAATTTATCTTTTCGCTACA 2553
Db 302 GACTGCGCATGTTAGCAGAGAAACAGCATCAACAGGAATTTATCTTTTCGCTACA 361
Qy 2554 CAAAGTAGCCCATCTGCTCATTTTGAACCTGTGGGAAGCTCGTCTATCAGCATGATGCT 2613
Db 362 CAAAGTAGCCCATCTGCTCATTTTGAACCTGTGGGAAGCTCGTCTATCAGCATGATGCT 421
Qy 2614 GATCTTGAATCCCTGCTGCTGCTTGAAGAGATTTGGAGAGACACACAGAACTCTCA 2673
Db 422 GACCTGACCTCCCTGCTGCTGCTTGGAGAGATAGGAAGGACACACACTTAAATCTCA 481
Qy 2674 AACATTTGAGATCCAGCTTGTATGAGCGGACTTCAACTACAGCGGCAAAATGACATC 2733
Db 482 GACATAACAGAGACTGAGATCGAGGAGCTGCTCACTTCACTACAGCAGACAAAATGACAT 541
Qy 2734 TAG 2736
Db 542 TAG 544

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 23:03:03 ; Search time 1371 Seconds  
(without alignments)  
11813.576 Million cell updates/sec

Title: US-10-798-721-9  
Perfect score: 2736  
Sequence: 1 atggggagagcggcgccac.....gcaggcaaatggactctag 2736

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 16Dec04:\*  
1: Geneseqn19808:\*  
2: Geneseqn19908:\*  
3: Geneseqn20008:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2736	100.0	2736	13	ADR44586 Novel hum
2	2736	100.0	3411	13	ADR44584 Novel hum
3	2660	97.2	2703	13	ADR44588 Novel hum
4	2642	96.6	2694	13	ADR44590 Novel hum
5	2566	93.8	2661	13	ADR44592 Novel hum
6	2365.2	86.4	7002	6	ABK88064 cDNA enco
7	2365.2	86.4	7002	13	ADP56230 Human PRO
8	2320.8	84.8	8899	12	ADQ24624 Human sof
9	2287	83.6	2979	10	ABX17909 cDNA enco
10	2284	83.5	2868	10	ADC77423 Human tra
11	2260	82.6	2898	8	ABX70459 DNA enco
12	2260	82.6	2898	12	ADL24070 Human NOV
13	2220	81.1	2661	10	ADC77421 Human tra
14	2043	74.7	2043	13	ADR44602 Novel hum
15	1967	71.9	2010	13	ADR44604 Novel hum
16	1949	71.2	2001	13	ADR44606 Novel hum
17	1873	68.5	1968	13	ADR44608 Novel hum
18	1640	59.9	1734	13	ADR44578 Novel hum
19	1599.8	58.5	2448	12	ADQ63069 Novel hum
20	1564	57.2	1701	13	ADR44580 Novel hum

21	1546	56.5	1692	13	ADR44582	Novel hum
22	1470	53.7	1659	13	ADR44584	Novel hum
23	947	34.6	1041	13	ADR44594	Novel hum
24	871	31.8	1008	13	ADR44596	Novel hum
25	867.8	31.7	2181	8	ABX70460	DNA enco
26	867.8	31.7	2181	12	ADL24072	Human NOV
27	853	31.2	999	13	ADR44598	Novel hum
28	777	28.4	966	13	ADR44600	Novel hum
29	638.4	23.3	2595	12	ADQ63623	Novel hum
30	597	21.8	2860	6	ABT06279	Human NOV
31	592.2	21.6	2860	6	ABT06280	Human NOV
32	590.2	21.6	3933	13	ADR07892	Full leng
33	588.6	21.5	3884	4	AAS21316	Human CDN
34	588.6	21.5	3884	4	ACA03675	cDNA enco
35	588.6	21.5	3884	8	ABX89213	DNA enco
36	588.6	21.5	3884	8	ACD41867	Human sec
37	588.6	21.5	3884	8	ACA04096	Human CDN
38	588.6	21.5	3884	9	ADA45664	Novel hum
39	588.6	21.5	3884	9	ADA76095	Human PRO
40	588.6	21.5	3884	9	ADA18745	Human PRO
41	588.6	21.5	3884	9	ADA61368	Homo sapi
42	588.6	21.5	3884	9	ADB19153	Novel hum
43	588.6	21.5	3884	9	ADB27694	cDNA enco
44	588.6	21.5	3884	9	ADA86173	Novel hum
45	588.6	21.5	3884	9	ADB15737	Human PRO

## ALIGNMENTS

RESULT 1  
ADR44586  
ID ADR44586 standard; cDNA; 2736 BP.  
XX  
AC ADR44586;  
DT 04-NOV-2004 (first entry)  
XX  
DE Novel human protein (NHP) encoding cDNA #5.  
XX  
KW Novel human protein; NHP; drug screening; clinical trial monitoring;  
KW cancer; arthritis; cosmetic application; cytostatic; virucidal;  
KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;  
KW gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 1..2736  
FT /\*tag= a  
FT /product= "Novel human protein (NHP)"  
FT replace(776,C)  
FT /\*tag= b  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
FT replace(788,C)  
FT /\*tag= c  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
FT replace(1276,T)  
FT /\*tag= d  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
US6777232-B1.  
FN  
XX  
PD 17-AUG-2004.  
XX  
PF 02-OCT-2001; 2001US-00969532.  
XX  
PR 02-OCT-2000; 2000US-0237280P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Walke DW, Scoville J;

DR WPI; 2004-591302/57.  
DR P-PSDB; ADR44587.  
XX New isolated human proteins and nucleic acids, useful for diagnosing,  
PT drug screening, clinical trial monitoring, or treating diseases and  
PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.  
XX  
PS Claim 1; SEQ ID NO 9; 52pp; English.  
XX  
CC The present invention provides novel human proteins (NHPs) and their  
CC encoding polynucleotides. The invention is useful for diagnosis, drug  
CC screening, clinical trial monitoring, treatment of diseases and disorders  
CC such as cancer and arthritis and cosmetic applications. The invention  
CC acts as a cytostatic and virucidal agent. The invention is useful in gene  
CC therapy. The present sequence is a novel human protein (NHP) encoding  
CC cDNA. The NHP encoding cDNA is located on human chromosome 8.  
XX  
SQ Sequence 2736 BP; 713 A; 715 C; 695 G; 613 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 2736; DB 13; Length 2736;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGGGAGAGCGCGCCACCGCAGCGCGCGGAGGCGCGCGCTCGCTCCCGTGG 60  
DB 1 ATGGGAGAGCGCGCGCCACCGCAGCGCGCGGAGGCGCGCGCTCGCTCCCGTGG 60  
  
QY 61 CTGGGGCTGTCTTCTGGGGCGGAGGAGCGCGCGCTGCGGAGAACTGACATGCGGAA 120  
DB 61 CTGGGGCTGTCTTCTGGGGCGGAGGAGCGCGCGCTGCGGAGAACTGACATGCGGAA 120  
  
QY 121 GCCTTCCCAATCCATCCATCAGCTCTCTGGGACACTGCTCATTTTATAGAGGAGCCA 180  
DB 121 GCCTTCCCAATCCATCCATCAGCTCTCTGGGACACTGCTCATTTTATAGAGGAGCCA 180  
  
QY 181 GATGATCTTATATATCAAGAGCAACCCCTATTGCACTCAGGTGCAAGCGAGCGCGC 240  
DB 181 GATGATCTTATATATCAAGAGCAACCCCTATTGCACTCAGGTGCAAGCGAGCGCGC 240  
  
QY 241 ATGCAGATATTTCTCAATGCAACGGGAGTGGTCCATCAGACGAGCACTCTGGA 300  
DB 241 ATGCAGATATTTCTCAATGCAACGGGAGTGGTCCATCAGACGAGCACTCTGGA 300  
  
QY 301 GAGACTCTGAGAGAGCTCAGGTTTGAAGTCCGCGAGTGTTCATCAATGTTACTAGG 360  
DB 301 GAGACTCTGAGAGAGCTCAGGTTTGAAGTCCGCGAGTGTTCATCAATGTTACTAGG 360  
  
QY 361 CAACAGGTGAGGACTTCCATGGGCGGAGGACTATTGGTCCAGTGTGGCGTGGAGC 420  
DB 361 CAACAGGTGAGGACTTCCATGGGCGGAGGACTATTGGTCCAGTGTGGCGTGGAGC 420  
  
QY 421 CACTGGGTACCTCCAGAGCGAGGAGGCTCTGTGCGCATAGCTATTATTTACGGAAGAAC 480  
DB 421 CACTGGGTACCTCCAGAGCGAGGAGGCTCTGTGCGCATAGCTATTATTTACGGAAGAAC 480  
  
QY 481 TTTGAAACAAGACCCACAGGAAGGAAAGTTCCCATTTGAAGGCAATGTTACTGCACTGC 540  
DB 481 TTTGAAACAAGACCCACAGGAAGGAAAGTTCCCATTTGAAGGCAATGTTACTGCACTGC 540  
  
QY 541 CGCCCAACAGAGGAGTCCCTGTGCGGAGTGGAAATGGCTGAAAATGAAGGCCCATTT 600  
DB 541 CGCCCAACAGAGGAGTCCCTGTGCGGAGTGGAAATGGCTGAAAATGAAGGCCCATTT 600  
  
QY 601 GACTCTGAACAAGACGAGAACATTGACACAGGAGGCTGACCATTAACCTGATCATCAGGCGAG 660  
DB 601 GACTCTGAACAAGACGAGAACATTGACACAGGAGGCTGACCATTAACCTGATCATCAGGCGAG 660  
  
QY 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGCAATGGAGCGCAACATCTGGCTTAAGAGG 720  
DB 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGCAATGGAGCGCAACATCTGGCTTAAGAGG 720  
  
QY 721 AGAGCCTGTGCGGCACTTGTGCTCTACCTGATGGAGCTGGGAGTGTGAGCGGAA 780  
DB 721 AGAGCCTGTGCGGCACTTGTGCTCTACCTGATGGAGCTGGGAGTGTGAGCGGAA 780

DB 721 AGAGCCTGTGCGGCACTTGTGCTCTACCTGATGGAGCTGGGAGTGTGAGCGGAA 780  
QY 781 TGGTCCCTCTCCAGTCCAGAGTGTGAACATTTGGGATCCGGGATGTCACAGCACCACCC 840  
DB 781 TGGTCCCTCTCCAGTCCAGAGTGTGAACATTTGGGATCCGGGATGTCACAGCACCACCC 840  
QY 841 CCGAATAATGGGGCAAAATTTCTGTAAGGTCTAAGCCAGGAATCTGAAAATCTGCACAGAT 900  
DB 841 CCGAATAATGGGGCAAAATTTCTGTAAGGTCTAAGCCAGGAATCTGAAAATCTGCACAGAT 900  
QY 901 GGTCTTTCATCTAGATATAAAACCTTTCATGAAATAAAACCCCAAGCATTTAGAT 960  
DB 901 GGTCTTTCATCTAGATATAAAACCTTTCATGAAATAAAACCCCAAGCATTTAGAT 960  
QY 961 GCCAGCAGATTTGCTTCTACTCGGGCTTGGTCTGCTCGCTCGTGGCGTGTGCACTCTG 1020  
DB 961 GCCAGCAGATTTGCTTCTACTCGGGCTTGGTCTGCTCGCTCGTGGCGTGTGCACTCTG 1020  
QY 1021 GTCAATTGGTGTCAACCTTTTACAGAGCGGAGCGAGTGTATGCGTGGAGCTCATTTGAC 1080  
DB 1021 GTCAATTGGTGTCAACCTTTTACAGAGCGGAGCGAGTGTATGCGTGGAGCTCATTTGAC 1080  
QY 1081 TCTTCTGATTTGACAGGTGGCTTCCAGACCTTCACTTCAAAACAGTCCGTCACGCCAAG 1140  
DB 1081 TCTTCTGATTTGACAGGTGGCTTCCAGACCTTCACTTCAAAACAGTCCGTCACGCCAAG 1140  
QY 1141 AATATCATGGAACCTAATGATCAAGAAAAATCTCTTGGTAACTCCCTGCTCTGAAATCT 1200  
DB 1141 AATATCATGGAACCTAATGATCAAGAAAAATCTCTTGGTAACTCCCTGCTCTGAAATCT 1200  
QY 1201 GCCATGCGAGCGAGTCTGACAGTGGCGGACATACAGCGGAGCCCATCTGTCTGAGGAC 1260  
DB 1201 GCCATGCGAGCGAGTCTGACAGTGGCGGACATACAGCGGAGCCCATCTGTCTGAGGAC 1260  
QY 1261 CCTCTGCGACAGGAGCTCATGACAGTCTTAACTTTTAACTTTTGGGAGCATCAAA 1320  
DB 1261 CCTCTGCGACAGGAGCTCATGACAGTCTTAACTTTTAACTTTTGGGAGCATCAAA 1320  
QY 1321 GTGAAAGTCCAGAGCTCGTTTCAATGTTTCCCTGGGAGTGTCTGAGAGCTGAGTACCAC 1380  
DB 1321 GTGAAAGTCCAGAGCTCGTTTCAATGTTTCCCTGGGAGTGTCTGAGAGCTGAGTACCAC 1380  
QY 1381 GGCAGAAATCATTCAGGACTTTTCCCATGGAACCAACCAAGCATTTAGTACATGAT 1440  
DB 1381 GGCAGAAATCATTCAGGACTTTTCCCATGGAACCAACCAAGCATTTAGTACATGAT 1440  
QY 1441 CCCAGAAATATAATGCGCTTACATCAAAATCTGTCACTCCCAACAGGACAGAACTG 1500  
DB 1441 CCCAGAAATATAATGCGCTTACATCAAAATCTGTCACTCCCAACAGGACAGAACTG 1500  
QY 1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCGCAATACAGGGTG 1560  
DB 1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCGCAATACAGGGTG 1560  
QY 1561 AGCTTACTATACCAACAGCTGCCATCCAGAGGAGAAATCTTGGGAGATTTATATGTC 1620  
DB 1561 AGCTTACTATACCAACAGCTGCCATCCAGAGGAGAAATCTTGGGAGATTTATATGTC 1620  
QY 1621 ATCAACCAAGGTGAACCCAGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 1680  
DB 1621 ATCAACCAAGGTGAACCCAGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 1680  
QY 1681 GTCACTGTGGTCTCCAGACATGATGTCACCACTCCCTTTGCAATGACCATCCCGCAC 1740  
DB 1681 GTCACTGTGGTCTCCAGACATGATGTCACCACTCCCTTTGCAATGACCATCCCGCAC 1740  
QY 1741 TGTGAGAGTGTGAGTCTGAGCATTTGGAATATCCATTTAAGAGAGGACACAGCAGGGC 1800  
DB 1741 TGTGAGAGTGTGAGTCTGAGCATTTGGAATATCCATTTAAGAGAGGACACAGCAGGGC 1800  
QY 1801 AATATGGGAGAGTGTGATGTCAGTGGAGAGTGAATCTATCATCTGTTACTGCTTTTGGAC 1860  
DB 1801 AATATGGGAGAGTGTGATGTCAGTGGAGAGTGAATCTATCATCTGTTACTGCTTTTGGAC 1860



Db	595	TTTTGAAACAAGACCACAGAGAGGAAAGTTCCCATTTGAAGGCATGATGTACTGCACCTGC	1675	AGCTTACTCATACACACACGCGTGCCATCCAGAGAGAAATTTCTTGGGAGATTTATATATGCC	1734
Qy	541	CGCCACACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAATGAAGAGCCCAATT	1621	ATCAACCAAGGTGAAACCCAGCCTCCAGTCAGATGGCTCTCAGGTGCTCCTCAGTCTCTGAA	1680
Db	655	CGCCCAACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAATGAAGAGCCCAATT	1735	ATCAACCAAGGTGAAACCCAGCCTCCAGTCAGATGGCTCTCAGGTGCTCCTCAGTCTCTGAA	1794
Qy	601	GACTCTGAAACAAGACGAGAAATTTGACACACAGGGCTGACATTAACCTGATCATCAGGCAG	1681	GTCACTGTGTCTCTCAGACATGATCGTCACCACTCCCTTTTGCAATTTGACATCCCGAC	1740
Db	715	GACTCTGAAACAAGACGAGAAATTTGACACACAGGGCTGACATTAACCTGATCATCAGGCAG	1795	GTCACTGTGTCTCTCAGACATGATCGTCACCACTCCCTTTTGCAATTTGACATCCCGAC	1854
Qy	661	GCAAGCTCTCGACCTCAGGAATTTACCTCATCGCAGCCAAACATCTGTGCTAAGAGG	1741	TGTGAGATGTGCTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACACAGGCG	1800
Db	775	GCAAGCTCTCGACCTCAGGAATTTACCTCATCGCAGCCAAACATCTGTGCTAAGAGG	1855	TGTGAGATGTGCTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACACAGGCG	1914
Qy	721	AGAAGCTGTGCGCCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA	1801	AAATGGGAGGAGTGTGTCAGTGAAGAGAAATCTACATCTCTGTACTGCTTTTGGAC	1860
Db	835	AGAAGCTGTGCGCCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA	1915	AAATGGGAGGAGTGTGTCAGTGAAGAGAAATCTACATCTCTGTACTGCTTTTGGAC	1974
Qy	781	TGTCGCTGTGAGTCCAGAGTGTGAACATTTTCGGATCCGGAGTGCACAGCACCCACC	1861	CCCTTTGCGTGTCACTGTGCTCTGGAAGCTTTTGGACCTATGCGCTCACCTGGAGAGCCA	1920
Db	895	TGTCGCTGTGAGTCCAGAGTGTGAACATTTTCGGATCCGGAGTGCACAGCACCCACC	2034	CCCTTTGCGTGTCACTGTGCTCTGGAAGCTTTTGGACCTATGCGCTCACCTGGAGAGCCA	2094
Qy	841	CCGAGAAATCGGCGCAAAATTTCTGTAAGTCTTAAGCCAGGAATCTGAAAACCTGCACAGAT	1921	ATCACAGACTGTGCGGTGAAGCAACTGAAGTGGCGGTTTTTGGCTGCATGCTCTGTAAC	2040
Db	955	CCGAGAAATCGGCGCAAAATTTCTGTAAGTCTTAAGCCAGGAATCTGAAAACCTGCACAGAT	2094	ATCACAGACTGTGCGGTGAAGCAACTGAAGTGGCGGTTTTTGGCTGCATGCTCTGTAAC	2154
Qy	901	GGTCTTTGGCATCTAGATAAAAAACCTTTTCATGAATAAACCACCAAGCAATTTGAGAAAT	2041	GTGGTTTTCAGATGAAGGCATCAAGGTGGACAGCTCTTGGAGAACCAAAATTTGCTGCAT	2214
Db	1015	GGTCTTTGGCATCTAGATAAAAAACCTTTTCATGAATAAACCACCAAGCAATTTGAGAAAT	2155	GTGGTTTTCAGATGAAGGCATCAAGGTGGACAGCTCTTGGAGAACCAAAATTTGCTGCAT	2274
Qy	961	GCCAGCCACATTTGTTACTCGGCTTGGGTGCTGCGCTGCTGCGCTGTCAGTCTCTG	2101	TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCTTGTATTTCCCTCATTTCTCTGG	2220
Db	1075	GCCAGCCACATTTGTTACTCGGCTTGGGTGCTGCGCTGCTGCGCTGTCAGTCTCTG	2215	TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCTTGTATTTCCCTCATTTCTCTGG	2274
Qy	1021	GTCAATTTGGTGTACCTTTACAGACGGAGCCAGATGACTATGCGGTGGACGTCATTTGAC	2161	AGAATTAACCAATTCAGTCCCTGCGAGAAAGTCCCGTCTCCCGGTGTCGTCAGTAAAC	2334
Db	1135	GTCAATTTGGTGTACCTTTACAGACGGAGCCAGATGACTATGCGGTGGACGTCATTTGAC	2275	AGAATTAACCAATTCAGTCCCTGCGAGAAAGTCCCGTCTCCCGGTGTCGTCAGTAAAC	2394
Qy	1081	TCCTTCTGATGACAGTGGCTTCCAGACTTCAACTTTCAAAACAGTCCGTCAAGCCAAAG	2221	CGCGAGCCCTGACCTGTGCTTCTCCCTGGAGCGTTATAGCCCACTACCAACCCAGCTG	2340
Db	1195	TCCTTCTGATGACAGTGGCTTCCAGACTTCAACTTTCAAAACAGTCCGTCAAGCCAAAG	2335	CGCGAGCCCTGACCTGTGCTTCTCCCTGGAGCGTTATAGCCCACTACCAACCCAGCTG	2454
Qy	1141	AATATCATGGAACCTAATGATACAGAAAAATCCCTTTGGTAACTCCCTGCTCTCTGAAATCT	2281	TCCTGCAAAATCTGCATTTGCGAGCTCAAAGGCCATGAACAGATCTCTCAAGTGACAGCA	2400
Db	1255	AATATCATGGAACCTAATGATACAGAAAAATCCCTTTGGTAACTCCCTGCTCTCTGAAATCT	2395	TCCTGCAAAATCTGCATTTGCGAGCTCAAAGGCCATGAACAGATCTCTCAAGTGACAGCA	2514
Qy	1201	GCCATGACGACAGTCTGACAGTGGCGGACATACAGCGGACCCATCTGTCTGACGAGAC	2401	CTGTGACAGACTGGCCCCAAAGCCTTCAAAATTTCCCTACTCCATCAGACAGCGGATTTGT	2574
Db	1315	GCCATGACGACAGTCTGACAGTGGCGGACATACAGCGGACCCATCTGTCTGACGAGAC	2515	CTGTGACAGACTGGCCCCAAAGCCTTCAAAATTTCCCTACTCCATCAGACAGCGGATTTGT	2634
Qy	1261	CCTCTGGACAGGAGCTCATGACAGAGTCCCTCACTCTTTAACCCCTTTTGTGGACATCAAA	2461	GCTTACATTTTATAACCCCAATGCCCCAAAGGCAAGGCTGTCAGATTTAGCACAGAAAAAC	2520
Db	1375	CCTCTGGACAGGAGCTCATGACAGAGTCCCTCACTCTTTAACCCCTTTTGTGGACATCAAA	2575	GCTTACATTTTATAACCCCAATGCCCCAAAGGCAAGGCTGTCAGATTTAGCACAGAAAAAC	2694
Qy	1321	GTGAAAGTCCAGAGCTCGTTTCATGGTTTTCCCTGGGAGTGTCTGAGAGAGTGTGATCCAC	2521	AGCATCAACAGGAAATTTTATTTTTCGCTTACAAAGTAGGCCCATCTCTGTCATTTTGT	2640
Db	1435	GTGAAAGTCCAGAGCTCGTTTCATGGTTTTCCCTGGGAGTGTCTGAGAGAGTGTGATCCAC	2635	AGCATCAACAGGAAATTTTATTTTTCGCTTACAAAGTAGGCCCATCTCTGTCATTTTGT	2754
Qy	1381	GGCAAGATTCATTCAGAGCTTTTCCCATGGAAACCAACACAGCTTTTGTACATTCAT	2641	GAAGAGATTGGGAGGACACACAGAACTCTCAACATTTTCAGANTTTCCAGCTTTGATGAA	2700
Db	1495	GGCAAGATTCATTCAGAGCTTTTCCCATGGAAACCAACACAGCTTTTGTACATTCAT	2755	GAAGAGATTGGGAGGACACACAGAACTCTCAACATTTTCAGANTTTCCAGCTTTGATGAA	2814
Qy	1441	CCAGAAATTAATGCCCTTACATCCAAATCTGTCTCATCTCCCTCCCAAGGACAGAACTG			
Db	1555	CCAGAAATTAATGCCCTTACATCCAAATCTGTCTCATCTCCCTCCCAAGGACAGAACTG			
Qy	1501	AGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTG			
Db	1615	AGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTG			
Qy	1561	AGCTTACTCATACACAGGTCGCATCCAGAGGAGAAATCTTTGGGAGATTTATATGTCC			

QY 2701 GCCGACTTCACTACAGCAGGCAAAATGGACTCTAG 2736  
 Db 2815 GCCGACTTCACTACAGCAGGCAAAATGGACTCTAG 2850

RESULT 3

ADR44588  
 ID ADR44588 standard; cDNA; 2703 BP.

XX AC ADR44588;

XX DT 04-NOV-2004 (first entry)

XX DE Novel human protein (NHP) encoding cDNA #6.

XX KW Novel human protein; NHP; drug screening; clinical trial monitoring;  
 KW cancer; arthritis; cosmetic application; cytostatic; virucidal;  
 KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;  
 KW gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX CDS 1..2703

FT /tag= a  
 FT /product= "Novel human protein (NHP)"

FT variation replace(776,C)

FT /tag= b

FT variation /standard\_name= "Single nucleotide polymorphism (SNP)"

FT /tag= c

FT variation /standard\_name= "Single nucleotide polymorphism (SNP)"

FT /tag= d

FT variation /standard\_name= "Single nucleotide polymorphism (SNP)"

XX US6777232-B1.

XX 17-AUG-2004.

XX 02-OCT-2001; 2001US-00969532.

XX 02-OCT-2000; 2000US-0237280P.

XX (LEXI-) LEXICON GENETICS INC.

XX Walke DW, Scoville J;

XX WPI; 2004-591302/57.

XX P-PSDB; ADR44589.

XX New isolated human proteins and nucleic acids, useful for diagnosing,  
 PT drug screening, clinical trial monitoring, or treating diseases and  
 PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.

XX Disclosure; SEQ ID NO 11; 52pp; English.

XX The present invention provides novel human proteins (NHPs) and their  
 CC encoding polynucleotides. The invention is useful for diagnosis, drug  
 CC screening, clinical trial monitoring, treatment of diseases and disorders  
 CC such as cancer and arthritis and cosmetic applications. The invention  
 CC acts as a cytostatic and virucidal agent. The invention is useful in gene  
 CC therapy. The present sequence is a novel human protein (NHP) encoding  
 CC cDNA. The NHP encoding cDNA is located on human chromosome 8.

XX Sequence 2703 BP; 695 A; 707 C; 694 G; 607 T; 0 U; 0 Other;

XX Query Match 97.2%; Score 2660; DB 13; Length 2703;

XX Best Local Similarity 98.8%; Pred. No. 0;

XX Matches 2703; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 ATGGGGAGAGCGGCGGCCACCGCAGCGCGCGGCGCGCGCTCCCGTGG 60

1 ATGGGGAGAGCGGCGGCCACCGCAGCGCGCGGCGGCGCGCGCTCCCGTGG 60  
 61 CTGGGGCTGTGCTTCTGGGCGCGCAGGAGACCGCGGCTGCGCGAGGAACTGACAAATGGCGAA 120  
 61 CTGGGGCTGTGCTTCTGGGCGCGCAGGAGACCGCGGCTGCGCGAGGAACTGACAAATGGCGAA 120  
 121 GCCCTTCCGAAATCCATCCATCAGCTCTCTGGGACACATGGCTCATTTTATAGAGGAGCCA 180  
 121 GCCCTTCCGAAATCCATCCATCAGCTCTCTGGGACACATGGCTCATTTTATAGAGGAGCCA 180  
 181 GATGATGCTTATATATATCAAGAGCAACCTATTGGCACTCAGGTGCAAGAGCGAGCCAGGCC 240  
 181 GATGATGCTTATATATCAAGAGCAACCTATTGGCACTCAGGTGCAAGAGCGAGCCAGGCC 240  
 241 ATGCAGATATTTCTTCAAATGCAACGCGGAGTGGTCCATCAGAAACGAGCAGCTCTCTGAA 300  
 241 ATGCAGATATTTCTTCAAATGCAACGCGGAGTGGTCCATCAGAAACGAGCAGCTCTCTGAA 300  
 301 GAGACTCTGGAACGAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTACTAGG 360  
 301 GAGACTCTGGAACGAGAGCTCAGGTTTGAAGGTCGCGAAGTGTTCATCAATGTACTAGG 360  
 361 CAACAGGTGAGGACTTCCATGGGCGCGAGGACTATTGGTGCCAGTGTGGCGTGGAGC 420  
 361 CAACAGGTGAGGACTTCCATGGGCGCGAGGACTATTGGTGCCAGTGTGGCGTGGAGC 420  
 421 CACCTGGGTACCTCCAAAGAGCAGGAAGGCTCTGTGCGCATAGCTATTTACGGAAAAAC 480  
 421 CACCTGGGTACCTCCAAAGAGCAGGAAGGCTCTGTGCGCATAGCTATTTACGGAAAAAC 480  
 481 TTTGAAACAAGACCCACAAGAGGAAAGTTCCTTGAAGGCAATGATTTGCTGCACTGC 540  
 481 TTTGAAACAAGACCCACAAGAGGAAAGTTCCTTGAAGGCAATGATTTGCTGCACTGC 540  
 541 CGCCCAACAGAGGAGTCCCTGCTGCGAGGTGGATGGCTGAAATGAAGAGGCCCAT 600  
 541 CGCCCAACAGAGGAGTCCCTGCTGCGAGGTGGATGGCTGAAATGAAGAGGCCCAT 600  
 601 GACTCTGAAACAAGACCGAGAACATTGACACAGGCTGACCAATACCTGATCATCAGCAG 660  
 601 GACTCTGAAACAAGACCGAGAACATTGACACAGGCTGACCAATACCTGATCATCAGCAG 660  
 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGATGGCAGCCAACTGCTGGCTAGAGG 720  
 661 GCACGGCTCTCGGACTCAGGAAATTAACCTGATGGCAGCCAACTGCTGGCTAGAGG 720  
 721 AGAAGCCTGTCGCGCCACTGTTGGTCTACGTCGATGGGAGCTGGGAAGTGTGGAGCGAA 780  
 721 AGAAGCCTGTCGCGCCACTGTTGGTCTACGTCGATGGGAGCTGGGAAGTGTGGAGCGAA 780  
 781 TGCTCCGCTCTGCAAGTCCAGAGTGTGAACATTTTCGGATCCGGGAGTGCAAGCACCACCC 840  
 781 TGCTCCGCTCTGCAAGTCCAGAGTGTGAACATTTTCGGATCCGGGAGTGCAAGCACCACCC 840  
 841 CCAGAGAAATGGGGGCAAAATTTCTGAAAGGTCTAAGCCAGGAATCTGAAATCTGCACAGAT 900  
 841 CCAGAGAAATGGGGGCAAAATTTCTGAAAGGTCTAAGCCAGGAATCTGAAATCTGCACAGAT 900  
 901 GGCTTTTGCATCTTACATATAAAACCTCTTCATGAATAAAACCCCAAGCATTTGAGAAT 960  
 901 GGCTTTTGCATCTTACATATAAAACCTCTTCATGAATAAAACCCCAAGCATTTGAGAAT 960  
 961 GCCAGCGCAATTCCTTTGACTCGGGCTTGGGTGCTGCCCTCGTGGCGGTTGAGCGTCTG 1020  
 961 GCCAGCGCAATTCCTTTGACTCGGGCTTGGGTGCTGCCCTCGTGGCGGTTGAGCGTCTG 1020  
 981 GTCAATTTGGTGTACACCTTTACAGCGGAGCCAGAGTGAATATGGCGTGGAGCGTCAATGAC 1080  
 981 GTCAATTTGGTGTACACCTTTACAGCGGAGCCAGAGTGAATATGGCGTGGAGCGTCAATGAC 1080  
 1081 TCTTCTGCAATGACAGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCCTCAAGCCAG 1140  
 1081 TCTTCTGCAATGACAGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCCTCAAGCCAG 1140

Db 1048 TCTTCTGATGTGACAGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCCTCAAGCCAAG 1107  
 Qy 1141 AATATCATGAACTAATATACAAAGAAATCTTTGGTAACCTCCCTGCTCCCTGAATCT 1200  
 Db 1108 AATATCATGAACTAATATACAAAGAAATCTTTGGTAACCTCCCTGCTCCCTGAATCT 1167  
 Qy 1201 GCCATGAGCGAGATCTGACAGTGGAGCCGACATACAGCGGAGCCATCTCTGTCAGGAC 1260  
 Db 1168 GCCATGAGCGAGATCTGACAGTGGAGCCGACATACAGCGGAGCCATCTCTGTCAGGAC 1227  
 Qy 1261 CCTCTGGAAGAGCTCATGACAGAGTCTCTCTTAAACCTTTGTCGAGATCAAA 1320  
 Db 1228 CCTCTGGAAGAGCTCATGACAGAGTCTCTCTTAAACCTTTGTCGAGATCAAA 1287  
 Qy 1321 GTGAAAGTCCAGAGCTGTTTATGTTTCCCTGGAGTGTCTGAGAGCTGAGTACCA 1380  
 Db 1288 GTGAAAGTCCAGAGCTGTTTATGTTTCCCTGGAGTGTCTGAGAGCTGAGTACCA 1347  
 Qy 1381 GGCAAGATCATTTCCAGGACTTTTCCCATGGAACCAACACAGCTTTAGTACAATGCAT 1440  
 Db 1348 GGCAAGATCATTTCCAGGACTTTTCCCATGGAACCAACACAGCTTTAGTACAATGCAT 1407  
 Qy 1441 CCCAGAAATAAATGCCCTACATCCAAATCTGTCTCATCTCCCAAGAGGACAGACTG 1500  
 Db 1408 CCCAGAAATAAATGCCCTACATCCAAATCTGTCTCATCTCCCAAGAGGACAGACTG 1467  
 Qy 1501 AGGACAACTGCTGCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560  
 Db 1468 AGGACAACTGCTGCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1527  
 Qy 1561 AGCTTACTCATACACAGTGGCCATCCAGAGGAGAAATCTTTGGAGATTTATATGTCC 1620  
 Db 1528 AGCTTACTCATACACAGTGGCCATCCAGAGGAGAAATCTTTGGAGATTTATATGTCC 1587  
 Qy 1621 ATCAACCAAGTGAACCCAGCTCCAGTCCAGATGGCTCTGAGTGTCTCTGAGTCTGAA 1680  
 Db 1588 ATCAACCAAGTGAACCCAGCTCCAGTCCAGATGGCTCTGAGTGTCTCTGAGTCTGAA 1647  
 Qy 1681 GTCACTGTGCTCCTCAGACATGATCGTCCACACTCCCTTTTGCATTTGACCATCCCGCAC 1740  
 Db 1648 GTCACTGTGCTCCTCAGACATGATCGTCCACACTCCCTTTTGCATTTGACCATCCCGCAC 1707  
 Qy 1741 TGTGAGATGTGAGTCTGAGCATGGAATATCCATTTAAAGAGAGGACACAGCAGGGC 1800  
 Db 1708 TGTGAGATGTGAGTCTGAGCATGGAATATCCATTTAAAGAGAGGACACAGCAGGGC 1767  
 Qy 1801 AAATGGAGAGTGTGAGTCCAGTGGAGATGATCTACATCTCTTACTGCTTTGGAC 1860  
 Db 1768 AAATGGAGAGTGTGAGTCCAGTGGAGATGATCTACATCTCTTACTGCTTTGGAC 1827  
 Qy 1861 CCCTTTGCGTGTGATGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920  
 Db 1828 CCCTTTGCGTGTGATGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1887  
 Qy 1921 ATCAGACATGTGCGTGAAGCAATGAAAGTGGCGGTTTTTGGCTGCAATGCTCTGAAC 1980  
 Db 1888 ATCAGACATGTGCGTGAAGCAATGAAAGTGGCGGTTTTTGGCTGCAATGCTCTGAAC 1947  
 Qy 1981 TCCTCGAATTTACAACTTGAGATTTTACTGTGGAACATACCCCTTTGTCGATTTCAAGAA 2040  
 Db 1948 TCCTCGAATTTACAACTTGAGATTTTACTGTGGAACATACCCCTTTGTCGATTTCAAGAA 2007  
 Qy 2041 GTGGTTTTCAGATGAAAGGATCAAGTGGAGACCTCTCTGGAAGCAAAATTTGCTGCAT 2100  
 Db 2008 GTGGTTTTCAGATGAAAGGATCAAGTGGAGACCTCTCTGGAAGCAAAATTTGCTGCAT 2067  
 Qy 2101 TTCAAAGGGAATACCTTTAGTCTTCAAGATTTCTGCTTGAATTTCCCCCATTTCTCTGG 2160  
 Db 2068 TTCAAAGGGAATACCTTTAGTCTTCAAGATTTCTGCTTGAATTTCCCCCATTTCTCTGG 2127  
 Qy 2161 AGAATTTAAACCTTCACTGCTGCCAGGAGTCCCGTTCTCCGCGGTGTTGGTGCAGTAAC 2220  
 Db 2128 AGAATTTAAACCTTCACTGCTGCCAGGAGTCCCGTTCTCCGCGGTGTTGGTGCAGTAAC 2187

Qy 2221 CGGAGCCCTGCACTGTGCTTCTCCCTGGAGGTTTATACGCCCACTACCAACCCAGCTG 2280  
 Db 2188 CGGAGCCCTGCACTGTGCTTCTCCCTGGAGGTTTATACGCCCACTACCAACCCAGCTG 2247  
 Qy 2281 TCTGCAAAATCTGCAATTCGGCAGCTCAAAGGCAATGAAAGATCTTCAAGTGCAGACA 2340  
 Db 2248 TCTGCAAAATCTGCAATTCGGCAGCTCAAAGGCAATGAAAGATCTTCAAGTGCAGACA 2307  
 Qy 2341 TCAATCTAGAGAGTGAACGAGAAACCATCTTTCTTCCGCAACAGAGGACAGCACTTTC 2400  
 Db 2308 TCAATCTAGAGAGTGAACGAGAAACCATCTTTCTTCCGCAACAGAGGACAGCACTTTC 2367  
 Qy 2401 CTTGCAACAGCTGGCCCCCAAGCTTCAAAATTTCCCTACTTCCATCAGACAGCGATTTGT 2460  
 Db 2368 CTTGCAACAGCTGGCCCCCAAGCTTCAAAATTTCCCTACTTCCATCAGACAGCGATTTGT 2427  
 Qy 2461 GTTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCAGAGAAAC 2520  
 Db 2428 GTTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCAGAGAAAC 2487  
 Qy 2521 AGCATCAACAGGAATTTATCTTTTTCGCTACACAAAGTAGCCCATCTGCTGATTTTG 2580  
 Db 2488 AGCATCAACAGGAATTTATCTTTTTCGCTACACAAAGTAGCCCATCTGCTGATTTTG 2547  
 Qy 2581 AACCTGTGGGAAGCTCGTCTCATCAGCATGATGCTGATCTTGAATCTCCCTGGCTGCTGCTT 2640  
 Db 2548 AACCTGTGGGAAGCTCGTCTCATCAGCATGATGCTGATCTTGAATCTCCCTGGCTGCTGCTT 2607  
 Qy 2641 GAAGATTTGGGAGGACACACAGCAAACTCTCAAAATTTCAAAATTTCCAGATCCAGCTTGATGA 2700  
 Db 2608 GAAGATTTGGGAGGACACACAGCAAACTCTCAAAATTTCAAAATTTCCAGATCCAGCTTGATGA 2667  
 Qy 2701 GCGGACTTCACTACAGCAGGCAAAATGCACTCTAG 2736  
 Db 2668 GCGGACTTCACTACAGCAGGCAAAATGCACTCTAG 2703

RESULT 4  
 ADR44590  
 ID ADR44590 standard; cDNA; 2694 BP.  
 XX  
 AC ADR44590;  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE Novel human protein (NHP) encoding cDNA #7.  
 XX  
 KW Novel human protein; NHP; drug screening; clinical trial monitoring;  
 KW cancer; arthritis; cosmetic application; cytostatic; virucidal;  
 KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;  
 KW gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS  
 FT  
 FT Location/Qualifiers  
 FT 1..2694  
 FT /tag= a  
 FT /product= "Novel human protein (NHP)"  
 FT /replace= b  
 FT /tag= b  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 FT /replace(788,C)  
 FT /tag= c  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 FT /replace(1234,T)  
 FT /tag= d  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 PN US6777232-B1.  
 XX  
 PD 17-AUG-2004.  
 XX





QY 1741 TGTGACAGTGTCTGAGCATTGGAATATCCATTTTAAAGAGAGGACACAGCAGGCG 1800  
 DB 1699 TGTGACAGTGTCTGAGCATTGGAATATCCATTTTAAAGAGAGGACACAGCAGGCG 1758  
 QY 1801 AAATGGGAGAACTGATGTGAGTGGAGAGTAACTTACATCTCTGTTACTGCTTTTGGAC 1860  
 DB 1759 AAATGGGAGAACTGATGTGAGTGGAGAGTAACTTACATCTCTGTTACTGCTTTTGGAC 1818  
 QY 1861 CCCTTTGCGTGTCTGCTGAGCAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920  
 DB 1819 CCCTTTGCGTGTCTGCTGAGCAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1878  
 QY 1921 ATCAGAGATGTGCTGCTGAGCAACTGAAGTGGCGGTTTTTGGCTGCATGTCTCTTAAC 1980  
 DB 1879 ATCAGAGATGTGCTGCTGAGCAACTGAAGTGGCGGTTTTTGGCTGCATGTCTCTTAAC 1938  
 QY 1981 TCCCTGGATTAACTTTGAGAGTTTACTGTGTGGACAAATACCCCTTTGTGCAATTTACGAA 2040  
 DB 1939 TCCCTGGATTAACTTTGAGAGTTTACTGTGTGGACAAATACCCCTTTGTGCAATTTACGAA 1998  
 QY 2041 GTGCTTTCAGATGAAAGGATCAAGTGGGACAGCTCTCGGAGAACCAAAATTTGCTGCAT 2100  
 DB 1999 GTGCTTTCAGATGAAAGGATCAAGTGGGACAGCTCTCGGAGAACCAAAATTTGCTGCAT 2058  
 QY 2101 TTCAAAGGGGAATACCTTTAGTCTTTCAGATTCTGTCTTGTATTTCCCTCATTTCTCTG 2160  
 DB 2059 TTCAAAGGGGAATACCTTTAGTCTTTCAGATTCTGTCTTGTATTTCCCTCATTTCTCTG 2118  
 QY 2161 AGAATTAACCAATTCATGCTGCTGCGAGAAAGTCCCGTTCTCCGCTGTGGTGCATTAAC 2220  
 DB 2119 AGAATTAACCAATTCATGCTGCTGCGAGAAAGTCCCGTTCTCCGCTGTGGTGCATTAAC 2178  
 QY 2221 CGGAGCCCTGACATGCTGCTTCTCCCTGGAGGTTATACGCCCACTACCCAGCTG 2280  
 DB 2179 CGGAGCCCTGACATGCTGCTTCTCCCTGGAGGTTATACGCCCACTACCCAGCTG 2238  
 QY 2281 TCTGCAAAATCTGCAATTCGGCAGCTCAAGGCGCATGAACAGATCTCTCAAGTGCAGACA 2340  
 DB 2239 TCTGCAAAATCTGCAATTCGGCAGCTCAAGGCGCATGAACAGATCTCTCAAGTGCAGACA 2298  
 QY 2341 TCAATCTAGAGAGTGAACAGAGAAACATCATCTTTCTTGTGCAACAGAGGACAGCATTTTC 2400  
 DB 2299 TCAATCTAGAGAGTGAACAGAGAAACATCATCTTTCTTGTGCAACAGAGGACAGCATTTTC 2358  
 QY 2401 CCTGCAAGACTGCCCCAAGCTTCAAAATTTCCCTTCTCAATCAGACAGCGGATTTGT 2460  
 DB 2359 CCTGCAAGACTGCCCCAAGCTTCAAAATTTCCCTTCTCAATCAGACAGCGGATTTGT 2418  
 QY 2461 GCTACATTTGATACCCCAATGCCAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520  
 DB 2419 GCTACATTTGATACCCCAATGCCAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2478  
 QY 2521 AGCATCAAGAGAAATTTATCTTATTTTGTGCTACACAAAGTACCCATCTGCTGCTTTG 2580  
 DB 2479 AGCATCAAGAGAAATTTATCTTATTTTGTGCTACACAAAGTACCCATCTGCTGCTTTG 2538  
 QY 2581 AACCTGTGGGAAGCTGCTGATCAGCATGATGTTGATCTTCACTCCCTGGGCTGTGCGCTT 2640  
 DB 2539 AACCTGTGGGAAGCTGCTGATCAGCATGATGTTGATCTTCACTCCCTGGGCTGTGCGCTT 2598  
 QY 2641 GAAGAGATTGGGAGGACACACAGAAACTCTCAAAACATTTTCAAGATCCCAAGCTTGATGA 2700  
 DB 2599 GAAGAGATTGGGAGGACACACAGAAACTCTCAAAACATTTTCAAGATCCCAAGCTTGATGA 2658  
 QY 2701 GCGGACTTCACTACAGCAGGCAAAATGGACTCTAG 2736  
 DB 2659 GCGGACTTCACTACAGCAGGCAAAATGGACTCTAG 2694  
 RESULT 5  
 ADR44592  
 ID ADR44592 standard; cdna; 2661 BP.

XX ADR44592;  
 AC 04-NOV-2004 (first entry)  
 DT Novel human protein (NHP) encoding cDNA #8.  
 DE Novel human protein; NHP; drug screening; clinical trial monitoring;  
 KW cancer; arthritis; cosmetic application; cytostatic; virucidal;  
 KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;  
 KW Gene; SS.  
 XX Homo sapiens.  
 OS  
 XX Key  
 CDS 1..2661  
 FT /tag= a  
 FT /product= "Novel human protein (NHP)"  
 FT /replace(776,C)  
 FT /tag= b  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 FT /replace(788,C)  
 FT /tag= c  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 FT /replace(1201,T)  
 FT /tag= d  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 XX US6777232-B1.  
 PN 17-AUG-2004.  
 XX 02-OCT-2001; 2001US-00969532.  
 XX 02-OCT-2000; 2000US-0237280P.  
 PR (LEXI-) LEXICON GENETICS INC.  
 XX Walke DW, Scoville J;  
 PI WPI: 2004-591302/57.  
 DR P-PSDB; ADR44593.  
 DR  
 XX New isolated human proteins and nucleic acids, useful for diagnosing,  
 PT drug screening, clinical trial monitoring, or treating diseases and  
 PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.  
 XX Disclosure; SEQ ID NO 15; 52pp; English.  
 PS  
 XX The present invention provides novel human proteins (NHPs) and their  
 CC encoding polynucleotides. The invention is useful for diagnosis, drug  
 CC screening, clinical trial monitoring, treatment of diseases and disorders  
 CC such as cancer and arthritis and cosmetic applications. The invention  
 CC acts as a cytostatic and virucidal agent. The invention is useful in gene  
 CC therapy. The present sequence is a novel human protein (NHP) encoding  
 CC cDNA. The NHP encoding cDNA is located on human chromosome 8.  
 XX  
 SQ Sequence 2661 BP; 676 A; 700 C; 688 G; 597 T; 0 U; 0 Other;  
 Query Match 93.8%; Score 2566; DB 13; Length 2661;  
 Best Local Similarity 97.3%; Pred.No. 0;  
 Matches 2661; Conservative 0; Mismatches 0; Indels 75; Gaps 2;  
 QY 1 ATGGGGAGAGCGCGCCACCGCAGCGCGGCGGAGGGCGCGCGTGGCTCCCGTGG 60  
 DB 1 ATGGGGAGAGCGCGCCACCGCAGCGCGGCGGAGGGCGCGCGTGGCTCCCGTGG 60  
 QY 61 CTGGGGCTGTGCTTCTGGGGCGGAGGACCGGGCTGCCGAGGAATGCAATGGGAA 120  
 DB 61 CTGGGGCTGTGCTTCTGGGGCGGAGGACCGGGCTGCCGAGGAATGCAATGGGAA 120  
 QY 121 GCCCTTCCCGAATCCATCCATCAGCTCTCTGGGACACTGCCTCATTTATAGAGAGCCA 180

Db 121 GCCCTTCCCGAATCCATCCATCAGCTCCTGGGACACTGCCTCATTTTCATAGAGGCCA 180  
Qy 181 GATGATGCTTATATATCAAGAGAAACCCATTATTTGCACTCAGGTGCAAGCGAGCCAGCC 240  
Db 181 GATGATGCTTATATATCAAGAGAAACCCATTATTTGCACTCAGGTGCAAGCGAGCCAGCC 240  
Qy 241 ATCCAGATATTTCTCAAAATGCAACGGGAGTGGTCCATCAGAACCGAGCAGCTCTCTGA 300  
Db 241 ATCCAGATATTTCTCAAAATGCAACGGGAGTGGTCCATCAGAACCGAGCAGCTCTCTGA 300  
Qy 301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGTCCGGAGTGTTCATCAATGTTACTAGG 360  
Db 301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGTCCGGAGTGTTCATCAATGTTACTAGG 360  
Qy 361 CAACAGGTGAGAGCTTCCATGCGCCGAGGACTATTTGGTCCAGTGTGGCGTGGAGC 420  
Db 361 CAACAGGTGAGAGCTTCCATGCGCCGAGGACTATTTGGTCCAGTGTGGCGTGGAGC 420  
Qy 421 CACCTGGTACCTCCAAAGACAGAGGCTCTGTGGCAATAGCCTATTTACGGAAGAAC 480  
Db 421 CACCTGGTACCTCCAAAGACAGAGGCTCTGTGGCAATAGCCTATTTACGGAAGAAC 480  
Qy 481 TTTGAACAAGACCCACAAGGAAGGAAGTTCCCAATTTGAAGGCATGATTTGCTGCACTGC 540  
Db 481 TTTGAACAAGACCCACAAGGAAGGAAGTTCCCAATTTGAAGGCATGATTTGCTGCACTGC 540  
Qy 541 CGCCCAACAGAGGAGTCCCTGTCGCGAGTGGAAATGGCTGAATAAAGAGGCCCAT 600  
Db 541 CGCCCAACAGAGGAGTCCCTGTCGCGAGTGGAAATGGCTGAATAAAGAGGCCCAT 600  
Qy 601 GACTCTGAAACAGACAGAGCAATTTGACACAGGGCTGACCATTAACCTGATCATCAGGCAG 660  
Db 601 GACTCTGAAACAGACAGAGCAATTTGACACAGGGCTGACCATTAACCTGATCATCAGGCAG 660  
Qy 661 GCACGGCTCTCGGACTCAGGAATTAACCTGCATGCGCAGCAACATCGTGGCTGAAGAGG 720  
Db 661 GCACGGCTCTCGGACTCAGGAATTAACCTGCATGCGCAGCAACATCGTGGCTGAAGAGG 720  
Qy 721 AGAAGCCTGTCGCGCACTGTTGTGGTCTACGTGGATGGGAGTGGGAAGTGTGGAGCGAA 780  
Db 721 AGAAGCCTGTCGCGCACTGTTGTGGTCTACGTGGATGGGAGTGGGAAGTGTGGAGCGAA 780  
Qy 781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGCACACCC 840  
Db 781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGCACACCC 840  
Qy 841 CCGAGAAATGGGGCAAAATTTCTGTAAGGTCTAAGCCAGGAATCTGAAAACCTGCACAGAT 900  
Db 841 CCGAGAAATGGGGCAAAATTTCTGTAAGGTCTAAGCCAGGAATCTGAAAACCTGCACAGAT 900  
Qy 901 GGTCTTTGCACTTAGATAAAAAACCTCTTCAATGAATAAAAAACCCCAAGCAATTGAGAA 960  
Db 901 GGTCTTTGCACTTAG-----GCATTGAGAA 927  
Qy 961 GCCAGGCAATTTGCTTGTACTCGGGCTGGGTGCTGCGGTCTGGCGGTGCGAGTCCCTG 1020  
Db 928 GCCAGGCAATTTGCTTGTACTCGGGCTGGGTGCTGCGGTCTGGCGGTGCGAGTCCCTG 987  
Qy 1021 GTCAATTTGGTGTACCCCTTTACAGACGAGCCAGAGTGAATATGCGGTGGAAGTCAATTGAC 1080  
Db 988 GTCAATTTGGTGTACCCCTTTACAGACGAGCCAGAGTGAATATGCGGTGGAAGTCAATTGAC 1047  
Qy 1081 TCTTCTGCAATGACAGTGGCTTCCAGACCTTCAACTTCAAAAACAGTCCGTCAGGCCAAG 1140  
Db 1048 TCTTCTGCAATGACAGTGGCTTCCAGACCTTCAACTTCAAAAACAGTCCGTCAGGCCA 1101  
Qy 1141 AATATCATGGAATAATGATACAGAAAAATCCCTTTGGTAACTCCCTGCTCTCGAATTTCT 1200  
Db 1102 -----GGTAACCTCCCTGCTCTCGAATTTCT 1125  
Qy 1201 GCCATGACCCAGATCTGACAGTGAAGCCGACATACAGCGGACCCCATCTGCTCAGGAGC 1260  
Db 1126 GCCATGACCCAGATCTGACAGTGAAGCCGACATACAGCGGACCCCATCTGCTCAGGAGC 1185

Qy 1261 CCTCTGGAACAAGAGCTCATGACAGAGTCTCTCACTCTTTAAACCTTTGTTCGGACATCAAA 1320  
Db 1186 CCTCTGGAACAAGAGCTCATGACAGAGTCTCTCACTCTTTAAACCTTTGTTCGGACATCAAA 1245  
Qy 1321 GTGAAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTGTCTCAGAGAGCTGTAGTACCAC 1380  
Db 1246 GTGAAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTGTCTCAGAGAGCTGTAGTACCAC 1305  
Qy 1381 GSCAAGAATCATTTCCAGGACTTTTCCCATGGAACCAACACAGACTTTTACTACAATGCAT 1440  
Db 1306 GSCAAGAATCATTTCCAGGACTTTTCCCATGGAACCAACACAGACTTTTACTACAATGCAT 1365  
Qy 1441 CCCAGAAATAAATGCGCTACATCCAAAATCTGTCTCATCTCCCAACAGAGCAAGAACTG 1500  
Db 1366 CCCAGAAATAAATGCGCTACATCCAAAATCTGTCTCATCTCCCAACAGAGCAAGAACTG 1425  
Qy 1501 AGGACAACTGGTGTCTTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560  
Db 1426 AGGACAACTGGTGTCTTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1485  
Qy 1561 AGCTTACTCATACACACAGGTGCCATCCAGAGAGAGAAATTTCTTGGAGATTTATATGTCC 1620  
Db 1486 AGCTTACTCATACACACAGGTGCCATCCAGAGAGAGAAATTTCTTGGAGATTTATATGTCC 1545  
Qy 1621 ATCAACAAAGGTGAAACCCAGCTCCAGTCAAGATGGTCTCTGAGTGTCTCTGAGTCTTGAA 1680  
Db 1546 ATCAACAAAGGTGAAACCCAGCTCCAGTCAAGTGGTCTCTGAGTGTCTCTGAGTCTTGAA 1605  
Qy 1681 GTCACCTGTGGTCTCCAGACATGATCGTCAACCTCCCTTTCATTTGACATCCCGCAC 1740  
Db 1606 GTCACCTGTGGTCTCCAGACATGATCGTCAACCTCCCTTTCATTTGACATCCCGCAC 1665  
Qy 1741 TGTGACAGATGTCTGAGTATGGAATATCCATTTAAAGAGAGGACACAGCAGGGC 1800  
Db 1666 TGTGACAGATGTCTGAGTATGGAATATCCATTTAAAGAGAGGACACAGCAGGGC 1725  
Qy 1801 AAATGGAGAGAGTGAATGTCAGTGGAAAGTGAATCTACATCTGTTTCTGCTTTTGGAC 1860  
Db 1726 AAATGGAGAGAGTGAATGTCAGTGGAAAGTGAATCTACATCTGTTTCTGCTTTTGGAC 1785  
Qy 1861 CCTTTGCGTGTGTCATGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920  
Db 1786 CCTTTGCGTGTGTCATGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1845  
Qy 1921 ATCACAAGCTGTGCGCTGAAAGCAACTGAAAGTGGCGTCTTTGGCTGCTGCTCTGTAAC 1980  
Db 1846 ATCACAAGCTGTGCGCTGAAAGCAACTGAAAGTGGCGTCTTTGGCTGCTGCTCTGTAAC 1905  
Qy 1981 TCCCTGGATTAACAATTGAGAGTTTACTGTGTGGAACAATACCCCTTGTGCAATTCAGGAA 2040  
Db 1906 TCCCTGGATTAACAATTGAGAGTTTACTGTGTGGAACAATACCCCTTGTGCAATTCAGGAA 1965  
Qy 2041 GTGTTTTCAGATGAAGGACATCAAGTGGACAGCTCCTCGAGAAACCAAAATTTGCTGCAT 2100  
Db 1966 GTGTTTTCAGATGAAGGACATCAAGTGGACAGCTCCTCGAGAAACCAAAATTTGCTGCAT 2025  
Qy 2101 TTTCAAGGGAATACCTTTTGTAGTCTTTCAGATTTCTGCTCTTGTATTTCCCATTTCTCTGG 2160  
Db 2026 TTTCAAGGGAATACCTTTTGTAGTCTTTCAGATTTCTGCTCTTGTATTTCCCATTTCTCTGG 2085  
Qy 2161 AGAATTAACCAATTCATGCTGCTGCGGAGAGTCCCTTCTCCGCGTGTGGTGAAGTAAAC 2220  
Db 2086 AGAATTAACCAATTCATGCTGCTGCGGAGAGTCCCTTCTCCGCGTGTGGTGAAGTAAAC 2145  
Qy 2221 CGGAGCCCTGCACTGTGCTCTCCCTGGAGGCTTATACGCGCACTACCAACCCAGCTG 2280  
Db 2146 CGGAGCCCTGCACTGTGCTCTCCCTGGAGGCTTATACGCGCACTACCAACCCAGCTG 2205  
Qy 2281 TCTGCAAAATCTGCAATTCGAGCTCAAGAGGCAATGAACAGATCTCTCAAGTGCAGACA 2340  
Db 2206 TCTGCAAAATCTGCAATTCGAGCTCAAGAGGCAATGAACAGATCTCTCAAGTGCAGACA 2265



```
QY 947 AAAGCATTTGAGAAATGCCAGCGACATTCCTTTTGTACTCGGGCTTGGGTGCTGCGTGTGG 1006
DB 1155 AAAGCATTTGAGAAATGCCAGCGACATTCCTTTTGTACTCGGGCTTGGGTGCTGCGTGTGG 1214
QY 1007 CCGTTGCGAGTCCCTGGGTCAATTCCTTTACAGACGGAGCCAGAGTGACTATGGCG 1066
DB 1215 CCGTTGCGAGTCCCTGGGTCAATTCCTTTACAGACGGAGCCAGAGTGACTATGGCG 1274
QY 1067 TGAACGTCATGACTCTTCTGCAATGACAGGTGGCTTCCAGACTTCAACTTCAAAACAG 1126
DB 1275 TGAACGTCATGACTCTTCTGCAATGACAGGTGGCTTCCAGACTTCAACTTCAAAACAG 1334
QY 1127 TCCGTCAAGCCAGAAATATCATGGAACATATGATACAGAAAAATCCTTTGGTAACTCCC 1186
DB 1335 TCCGTCAA-----GGTAACTCCC 1352
QY 1187 TGCTCTCTGAATTTCTGCCATGACGCCAGTCTGACAGTGAGCCGAGACATACAGCGGACCCA 1246
DB 1353 TGCTCTCTGAATTTCTGCCATGACGCCAGTCTGACAGTGAGCCGAGACATACAGCGGACCCA 1412
QY 1247 TCTGTCTGCGAGCCCTCTGGACAAGGAGTCTATGACAGAGTCTCTCACTCTTTAAACCTTT 1306
DB 1413 TCTGTCTGCGAGCCCTCTGGACAAGGAGTCTATGACAGAGTCTCTCACTCTTTAAACCTTT 1472
QY 1307 TGTCCGACATCAAAAGTGAAAGTCCAGAGCTCGTTTCATGGTTTCCCTGGGAGTGTCTGAGA 1366
DB 1473 TGTCCGACATCAAAAGTGAAAGTCCAGAGCTCGTTTCATGGTTTCCCTGGGAGTGTCTGAGA 1532
QY 1367 GAGCTGAGTACCAAGCAAGAAATCATTCAGGAGCTTTTCCCATGGAACAAACACAGCT 1426
DB 1533 GAGCTGAGTACCAAGCAAGAAATCATTCAGGAGCTTTTCCCATGGAACAAACACAGCT 1592
QY 1427 TTAGTCAATGTCATCCAGAAAATAAAATGCCCTACATCCAAATCTGTCACTACTCCCCA 1486
DB 1593 TTAGTCAATGTCATCCAGAAAATAAAATGCCCTACATCCAAATCTGTCACTACTCCCCA 1652
QY 1487 CAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGC 1546
DB 1653 CAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGC 1712
QY 1547 CAAATACAGGGTGAGCTTACTCATACCAACAGTGCATCCAGAGGAGAAATCTTTGGG 1606
DB 1713 CAAATACAGGGTGAGCTTACTCATACCAACAGTGCATCCAGAGGAGAAATCTTTGGG 1772
QY 1607 AGATTTATATGTCATCAACCAAGGTGAACCCAGCTCCAGTCCAGATGGCTCTGAGGTGC 1666
DB 1773 AGATTTATATGTCATCAACCAAGGTGAACCCAGCTCCAGTCCAGATGGCTCTGAGGTGC 1832
QY 1667 TCTGAGTCTGAAAGTCACTGTGGTCTCTCCAGACATGATCGTCAACATCCCTTTTGCAT 1726
DB 1833 TCTGAGTCTGAAAGTCACTGTGGTCTCTCCAGACATGATCGTCAACATCCCTTTTGCAT 1892
QY 1727 TGACCATCCCGCACTGTCAGATGTCAAGTTCTGAGCAATTCGAATATCCATTTAAAGAGA 1786
DB 1893 TGACCATCCCGCACTGTCAGATGTCAAGTTCTGAGCAATTCGAATATCCATTTAAAGAGA 1952
QY 1787 GGACACAGCAGGGCAATGGGAGGAGTGTGATGTGAGTGAAGATGAATCTACATCCCTGTT 1846
DB 1953 GGACACAGCAGGGCAATGGGAGGAGTGTGATGTGAGTGAAGATGAATCTACATCCCTGTT 2012
QY 1847 ACTGCTTTTGGACCCCTTTTGGTGTCAATGTCTCTGGAACAGTTTGGACCTATGGCG 1906
DB 2013 ACTGCTTTTGGACCCCTTTTGGTGTCAATGTCTCTGGAACAGTTTGGACCTATGGCG 2072
QY 1907 TCACTGAGAGCCAAATCACAGACTGTGCGTGAAGCAACTGAAGTGGCGGTTTTTGGCT 1966
DB 2073 TCACTGAGAGCCAAATCACAGACTGTGCGTGAAGCAACTGAAGTGGCGGTTTTTGGCT 2132
QY 1967 GCATGCTCTGTAACCTCCCTGGATTAACAATTGAGAGTTTACTGTGTGGACAAATACCCCTT 2026
DB 2133 GCATGCTCTGTAACCTCCCTGGATTAACAATTGAGAGTTTACTGTGTGGACAAATACCCCTT 2192
```

```
2027 GTGCATTTTCAGGAAGTGGTTTTCAGATGAAAGGCATCAAGGTGACAGCTCTCTGGAAGAC 2086
2193 GTGCATTTTCAGGAAGTGGTTTTCAGATGAAAGGCATCAAGGTGACAGCTCTCTGGAAGAC 2252
2087 CAAATTTGCTGCAATTTCAAAGGGAATACCTTTTAGTCTTCAGATTTCTGTCTTGTATATTC 2146
2253 CAAATTTGCTGCAATTTCAAAGGGAATACCTTTTAGTCTTCAGATTTCTGTCTTGTATATTC 2312
2147 CCCATTTCTCTCGAGAAATTAACATTCATCTGCTGCGCCAGGAAGTCCCGTTCTCCGCG 2206
2313 CCCATTTCTCTCGAGAAATTAACATTCATCTGCTGCGCCAGGAAGTCCCGTTCTCCGCG 2372
2207 TGTGCTGCAATTAACCGGACCCCTGCACTGCTGCTTCTCCCTGGAGGCTTATACGCCCA 2266
2373 TGTGCTGCAATTAACCGGACCCCTGCACTGCTGCTTCTCCCTGGAGGCTTATACGCCCA 2432
2267 CTACACCCAGCTGCTCTGCAAAATCTGCAATTCGGCAGCTCAAGGCGCATGAACAGATCC 2326
2433 CTACACCCAGCTGCTCTGCAAAATCTGCAATTCGGCAGCTCAAGGCGCATGAACAGATCC 2492
2327 TCCAAGTGCAGACATCAATCTCTAGAGTGAAACGAGAAACCATCATCTTTCTTGCAAG 2386
2493 TCCAAGTGCAGACATCAATCTCTAGAGTGAAACGAGAAACCATCATCTTTCTTGCAAG 2552
2387 AGGACAGCACTTTCCCTGCGACAGCTGGCCCCCAAGCCTTCAAAATTTCCCTACTCCATCA 2446
2553 AGGACAGCACTTTCCCTGCGACAGCTGGCCCCCAAGCCTTCAAAATTTCCCTACTCCATCA 2612
2447 GACAGCGGATTTGCTGTCTACATTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGT 2506
2613 GACAGCGGATTTGCTGTCTACATTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGT 2672
2507 TAGCAGAGAAAAACAGATCAACAGGAATTTATCTTATTTTCGCTTACACAAAGTAGCCCAT 2566
2673 TAGCAGAGAAAAACAGATCAACAGGAATTTATCTTATTTTCGCTTACACAAAGTAGCCCAT 2732
2567 CTGCTCTCATTTTGAACCTGTGGGAAGCTCGTCACTAGCATGATGGTGTCTTGAATCTCC 2626
2733 CTGCTCTCATTTTGAACCTGTGGGAAGCTCGTCACTAGCATGATGGTGTCTTGAATCTCC 2792
2627 TGGCCCTGTGCCCCTTGAAGAGATTTGGGAGGACACACAGCAAACTCTCAAAATTTTCAAGT 2686
2793 TGGCCCTGTGCCCCTTGAAGAGATTTGGGAGGACACACAGCAAACTCTCAAAATTTTCAAGT 2852
2687 CCAGCTTGTATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
2853 CCAGCTTGTATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2902

RESULT 7
ADP56230
ID ADP56230 standard; cdna; 7002 BP.
XX
AC ADP56230;
XX
XX 18-NOV-2004 (first entry)
XX
Human PRO cDNA sequence SEQ ID NO:2206.
XX
human; PRO: immune related disease; inflammatory immune response;
immune response stimulation; antiallergic; antianemic; antiarthritic;
antirheumatic; antidiabetic; antiinflammatory; antipsoriatic;
antithrombotic; antihypertensive; CNS; dermatological; gastrointestinal;
haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
virucide; gene therapy; gene; ss.
XX
Homo sapiens.
XX
MO2004039956-A2.
XX
13-MAY-2004.
XX
```

28-OCT-2003; 2003WO-US034381.  
 29-OCT-2002; 2002US-0422472P.  
 (GETH ) GENENTECH INC.  
 Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;  
 Wood WI, Wu TD;  
 WPI; 2004-376182/35.  
 P-PSDB; ADP56231.  
 New PRO polynucleotides and polypeptides, useful in diagnosing  
 and treating an immune related disease, e.g. systemic lupus  
 erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
 stimulating an immune response.  
 Claim 2; SEQ ID NO 2206; 3009pp; English.  
 The present invention describes an isolated PRO nucleic acid (I). Also  
 described: (1) a vector comprising (I); (2) a host cell comprising the  
 vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
 isolated PRO polypeptide; (5) a chimeric molecule comprising the  
 polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
 antibody which specifically binds to a polypeptide of (4); (7) a  
 composition of matter comprising a polypeptide of (4), an agonist or  
 antagonist of the polypeptide or an antibody that binds to the  
 polypeptide in combination with a carrier; (8) an article of manufacture  
 comprising a container, a label on the container and a composition of  
 matter of (7); (9) a method of treating an immune related disease in a  
 mammal; (10) a method for determining the presence of a PRO polypeptide  
 in a sample suspected of having the polypeptide; (11) a method of  
 diagnosing an immune related disease or an inflammatory immune response  
 in mammal; (12) a method of identifying a compound that inhibits or  
 mimics the activity of or expression of a gene encoding a PRO polypeptide  
 ; and (13) a method of stimulating the immune response in a mammal. The  
 PRO sequences have anti-allergic, antianemic, antiarthritic,  
 antirheumatic, antidiabetic, anti-inflammatory, antipsoriatic,  
 antithyroid, CNS, dermatological, gastrointestinal,  
 haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,  
 nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and  
 virulence activities, and can be used in gene therapy. The nucleic acid  
 (I) and the encoded polypeptides, compositions, kits and methods are  
 useful in diagnosing and treating an immune related disease and in  
 stimulating an immune response. The present sequence represents a human  
 PRO nucleotide sequence from the present invention.  
 Sequence 7002 BP; 1989 A; 1491 C; 1499 G; 2023 T; 0 U; 0 Other;  
 Query Match 86.4%; Score 2365.2; DB 13; Length 7002;  
 Best Local Similarity 92.4%; Pred. No. 0;  
 Matches 2597; Conservative 0; Mismatches 3; Indels 210; Gaps 2;  
 95 CTGCCCAGGAACGTGACAAATGGGAGCCCTCCCGAATCCATCCCATGCTCCCTGGGA 154  
 135 CTTTCCAGGAACGTGACAAATGGGAGCCCTCCCGAATCCATCCCATGCTCCCTGGGA 194  
 155 CACTGCTCATTTTCATAGAGAGCCAGATGCTTATATATATATATATATATATATATAT 214  
 195 CACTGCTCATTTTCATAGAGAGCCAGATGCTTATATATATATATATATATATATATAT 254  
 215 CACTCAGGTGCAAGCGAGGCCAGCCATGCAGATATTTCTTCAAATGCAACGGCGAGTGG 274  
 255 CACTCAGGTGCAAGCGAGGCCAGCCATGCAGATATTTCTTCAAATGCAACGGCGAGTGG 314  
 275 TCCATCAGACGAGCAGTCTCTGACAGACTCTGGACGAGCTCAGGTTTGAAGTCC 334  
 315 TCCATCAGACGAGCAGTCTCTGACAGACTCTGGACGAGCTCAGGTTTGAAGTCC 374  
 335 GCGAAGTGTTCATCAATGTTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACT 394  
 375 GCGAAGTGTTCATCAATGTTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACT 434

QY 395 ATTGGTCCAGTGTGTGGCTGGAGCCCACTGGGTACTCTCAAGAGCAGGAAGGCTCTGT 454  
 DB 435 ATTGGTCCAGTGTGTGGCTGGAGCCCACTGGGTACTCTCAAGAGCAGGAAGGCTCTGT 494  
 QY 455 TCGCATAGCTTATTACGAAAAAATTGTAACAGACCCCAAGGAAGGAGTTCCCA 514  
 DB 495 TCGCATAGCTTATTACGAAAAAATTGTAACAGACCCCAAGGAAGGAGTTCCCA 554  
 QY 515 TTGAAGGATGATTTGCTACTGCTCCGCCCAACAGAGGAGTCCCTGCTGCCGAGGTGG 574  
 DB 555 TTGAAGGATGATTTGCTACTGCTCCGCCCAACAGAGGAGTCCCTGCTGCCGAGGTGG 614  
 QY 575 AATGCTGAAAAAATGAAGAGCCCATGACTCTGAAACAAGACGAGAACATTGACACAGGG 634  
 DB 615 AATGCTGAAAAAATGAAGAGCCCATGACTCTGAAACAAGACGAGAACATTGACACAGGG 674  
 QY 635 CTGACCATTAACCTGATCATCAGGAGGACCGCTCTCGGACTCAGGAATTAACCTGCA 694  
 DB 675 CTGACCATTAACCTGATCATCAGGAGGACCGCTCTCGGACTCAGGAATTAACCTGCA 734  
 QY 695 TGGCAGCCAAACATCTGGCTAAGAGAGAGAGCTCTCGGCCACTGTTGTGTCTAC- 750  
 DB 735 TGGCAGCCAAACATCTGGCTAAGAGAGAGAGCTCTCGGCCACTGTTGTGTCTACGTGA 794  
 QY 751 ----- 750  
 DB 795 ATGGAGGCTGTGTTCTCTGGACAGAGTGTGAGCTGCAATGTTGCTGTGTAGAGGAT 854  
 QY 751 ----- 750  
 DB 855 GGCAGAAAGTTCCCGGACCTGCACCAACCCAGCTCTCTCAATGGTGGGGCTTTTGTG 914  
 QY 751 -----GTGGATGGAGCTGGG 766  
 DB 915 AGGATGTCTAGTGAGAAAAAATCCTGACACTTCTTTTGTCTCTGTGGATGGAGCTGG 974  
 QY 767 AAGTGTGAGCGAATGTTGCTGCTGAGTGCAGAGTGTGAACATTTGCGATCCGGAGT 826  
 DB 975 AAGTGTGAGCGAATGTTGCTGCTGAGTGCAGAGTGTGAACATTTGCGATCCGGAGT 1034  
 QY 827 GCACAGCACCCCGGAGAAATGGGGCAAAATCTGCAAGGTCTTAAGCCAGGAATCTG 886  
 DB 1035 GCACAGCACCCCGGAGAAATGGGGCAAAATCTGCAAGGTCTTAAGCCAGGAATCTG 1094  
 QY 887 AAAAAGTGCAGATGCTTTTGCATCTAGATAAAAAACCTCTTCAATGAAAAAACC 946  
 DB 1095 AAAAAGTGCAGATGCTTTTGCATCTAGATAAAAAACCTCTTCAATGAAAAAACC 1154  
 QY 947 AAGCATTTGAGATGCGCAGCAGATGCTTTGCTCTCGGGCTTGGGTGCTCGCTCGTGG 1006  
 DB 1155 AAGCATTTGAGATGCGCAGCAGATGCTTTGCTCTCGGGCTTGGGTGCTCGCTCGTGG 1214  
 QY 1007 "CGTTGTCAGTCTGGTTCATTGGTGTCACTTGTCTCGGGCTTGGGTGCTCGCTCGTGG 1066  
 DB 1215 CGTTGTCAGTCTGGTTCATTGGTGTCACTTGTCTCGGGCTTGGGTGCTCGCTCGTGG 1274  
 QY 1067 TGGACGTCATTGATCTTCTGCTGATTTGACAGGTGGTTCAGACCTTTCAAATTCAAACAG 1126  
 DB 1275 TGGACGTCATTGATCTTCTGCTGATTTGACAGGTGGTTCAGACCTTTCAAATTCAAACAG 1334  
 QY 1127 TCGGTCAAGCCCAAGATATATATGGAATATATGGAATATATGGAATATATGGAATAT 1186  
 DB 1335 TCGGTCAAGCCCAAGATATATATGGAATATATGGAATATATGGAATATATGGAATAT 1352  
 QY 1187 TGTCTCTGAAATTTGCTGATGCGCAGCCAGATCTGACAGTGGAGCCGGAATACAGCGGACCCA 1246  
 DB 1353 TGTCTCTGAAATTTGCTGATGCGCAGCCAGATCTGACAGTGGAGCCGGAATACAGCGGACCCA 1412  
 QY 1247 TGTGTCTGAGGACCTCTGGAACAAGAGCTCATATGACAGAGTCTCACTCTTTAAACCTTT 1306  
 DB 1413 TGTGTCTGAGGACCTCTGGAACAAGAGCTCATATGACAGAGTCTCACTCTTTAAACCTTT 1472  
 QY 1307 TGTGCGACATCAAGATGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTGTCTGAGA 1366



Db 1473 TGTCGGACATCAAAAGTGAAGTCCAGAGCTCGTTTCATGGTTTCCTGGAGTGTCTGAGA 1532  
Qy 1367 GAGCTGAGTACCAACGGAAGATCATTTCCAGGAGCTTTTCCCCATGGAAACAAACACAGCT 1426  
Db 1533 GAGCTGAGTACCAACGGAAGATCATTTCCAGGAGCTTTTCCCCATGGAAACAAACACAGCT 1592  
Qy 1427 TTAGTCAATGCAATCCAGAAATAAATGCGCTTACATCCAAATCTGTCTATCTCCCA 1486  
Db 1593 TTAGTCAATGCAATCCAGAAATAAATGCGCTTACATCCAAATCTGTCTATCTCCCA 1652  
Qy 1487 CAAGGACAGAACTGAGGACAACTGGTCTTTTGGCCATTTAGGGGGCGCTTATGATATGC 1546  
Db 1653 CAAGGACAGAACTGAGGACAACTGGTCTTTTGGCCATTTAGGGGGCGCTTATGATATGC 1712  
Qy 1547 CAAATACAGGGGTGAGCTTACTCATACCAACACCGTGCCATCCAGAGGAGAAATCTTGGG 1606  
Db 1713 CAAATAACGGGGTGAGCTTACTCATACCAACACCGTGCCATCCAGAGGAGAAATCTTGGG 1772  
Qy 1607 AGATTTATATGTCATCAACCAAGGTGAACCCAGAGCTCCAGTCAGATGGCTCTGAGGTGC 1666  
Db 1773 AGATTTATATGTCATCAACCAAGGTGAACCCAGAGCTCCAGTCAGATGGCTCTGAGGTGC 1832  
Qy 1667 TCCTGAGTCCCTGAAGTCAACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTGTCAT 1726  
Db 1833 TCCTGAGTCCCTGAAGTCAACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTGTCAT 1892  
Qy 1727 TGACCATCCCGCACTGTGCAGATGTCTAGTTCTGAGCAATGGAAATATCCATTTAAAGAA 1786  
Db 1893 TGACCATCCCGCACTGTGCAGATGTCTAGTTCTGAGCAATGGAAATATCCATTTAAAGAA 1952  
Qy 1787 GGCACACAGAGGCAATGGAGAGAGTGTATGTCAGTGAAGATGAATCTACATCTCTGTT 1846  
Db 1953 GGCACACAGAGGCAATGGAGAGAGTGTATGTCAGTGAAGATGAATCTACATCTCTGTT 2012  
Qy 1847 ACTGCTTTTGGACCCCTTTGCGTGTCTGTCATGTCCTGACAGCTTTGGACCTATGCGC 1906  
Db 2013 ACTGCTTTTGGACCCCTTTGCGTGTCTGTCATGTCCTGACAGCTTTGGACCTATGCGC 2072  
Qy 1907 TCACTGAGAGCCCAATCACAGACTGTGCGCTGAAGCAACTGAAGGTGGCGGTTTTGGCT 1966  
Db 2073 TCACTGAGAGCCCAATCACAGACTGTGCGCTGAAGCAACTGAAGGTGGCGGTTTTGGCT 2132  
Qy 1967 GCATGCTCTGTAATCTCCCTGGATTAACATTTGAGAGTTTACTGTGTGGAACAATACCCCTT 2026  
Db 2133 GCATGCTCTGTAATCTCCCTGGATTAACATTTGAGAGTTTACTGTGTGGAACAATACCCCTT 2192  
Qy 2027 GTGCATTTACAGGAAGTGTTCAGATGAAGGATCAAGGTGGACAGCTCTCTGGAAGAAC 2086  
Db 2193 GTGCATTTACAGGAAGTGTTCAGATGAAGGATCAAGGTGGACAGCTCTCTGGAAGAAC 2252  
Qy 2087 CAAAATTTGCTGCAATTTCAAGGGAATACCTTTTGTCTCTTTCAGATTTCTGCTTGTATATTC 2146  
Db 2253 CAAAATTTGCTGCAATTTCAAGGGAATACCTTTTGTCTCTTTCAGATTTCTGCTTGTATATTC 2312  
Qy 2147 CCCCATTTCTGAGAAATTAACCAATTCATGCTGCCAGGAAGTCCCGTTCTCCGCG 2206  
Db 2313 CCCCATTTCTGAGAAATTAACCAATTCATGCTGCCAGGAAGTCCCGTTCTCCGCG 2372  
Qy 2207 TGTGTTGCAATACCCGACGCGCTTCAGCTGTGCTTCTCCCTGGAGCGTTATACGCCCA 2266  
Db 2373 TGTGTTGCAATACCCGACGCGCTTCAGCTGTGCTTCTCCCTGGAGCGTTATACGCCCA 2432  
Qy 2267 CTACCAACCCAGCTGTCTCGAAAATTCGCAATTCGGCAGCTCAAGGCGCATGAACAGATCC 2326  
Db 2433 CTACCAACCCAGCTGTCTCGAAAATTCGCAATTCGGCAGCTCAAGGCGCATGAACAGATCC 2492  
Qy 2327 TCCAAGTGCAGACATCAATCTTAGAGAGTGAACGAGAAACCATCTTCTTCGCAAG 2386  
Db 2493 TCCAAGTGCAGACATCAATCTTAGAGAGTGAACGAGAAACCATCTTCTTCGCAAG 2552  
Qy 2387 AGACAGCACTTTCCCTGCAACAGCTGGGCCCAAGGCTTCAAAATTCCTACTCATCA 2446

Db 2553 AGACAGCACTTTCCCTGCAACAGACTGGCCCCAAGCCTTCAAAATTCCTACTCATCA 2612  
Qy 2447 GACAGCGGATTTGTGCTACATTTTATACCCCAATGCAAAAGGCAAGGACTGGCAGATGT 2506  
Db 2613 GACAGCGGATTTGTGCTACATTTTATACCCCAATGCAAAAGGCAAGGACTGGCAGATGT 2672  
Qy 2507 TAGCACAGAAAACAGCATCAACAGGAATTTATCTTATTTTGGCTACACAAGTAGCCCAT 2566  
Db 2673 TAGCACAGAAAACAGCATCAACAGGAATTTATCTTATTTTCGTACACAAGTAGCCCAT 2732  
Qy 2567 CTCTGCTCATTTTGAACCTGTGGGAAGTCTCATCAGCATGATGGTGATCTTTGACTCCC 2626  
Db 2733 CTCTGCTCATTTTGAACCTGTGGGAAGTCTCATCAGCATGATGGTGATCTTTGACTCCC 2792  
Qy 2627 TGCCCTGTGCTTGAAGAGATTTGGAGGACACACAGAACTCTCAAAATTTTCAAGAT 2686  
Db 2793 TGCCCTGTGCTTGAAGAGATTTGGAGGACACACAGAACTCTCAAAATTTCAAGAT 2852  
Qy 2687 CCCAGCTTGATGAGCGGACTTCAACTACAGCAGGCAAAATGCACTCTAG 2736  
Db 2853 CCCAGCTTGATGAGCGGACTTCAACTACAGCAGGCAAAATGCACTCTAG 2902

RESULT 8  
ADQ24624  
ID ADQ24624 standard; DNA; 8899 BP.  
XX  
AC ADQ24624;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7444.  
XX  
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;  
KW ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2004048938-A2.  
XX  
PD 10-JUN-2004.  
XX  
PF 26-NOV-2003; 2003WO-US038193.  
XX  
PR 26-NOV-2002; 2002US-0429739P.  
XX  
PA (PROT-) PROTEIN DESIGN LABS INC.  
XX  
PI Aziz N, Ginsburg WM, Zlotnik A;  
XX  
WPI; 2004-441208/41.  
XX  
PT Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.  
XX  
PS Example 2; SEQ ID NO 7444; 210pp; English.  
XX  
CC The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in both soft tissue samples, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytostatic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC DNA of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.  
XX



QY 2021 CCCCTGTCATTTTCAGGAGTGGTTTCAGATGAAGGCATCAAGTGGACAGCTCCTGG 2080  
 Db 2187 NNNCTTGTGATTTTCAGAAAGTGGTTTCAGATGAAGGCATCAAGTGGACAGCTCCTGG 2246  
 QY 2081 AAGAACCAAAATTTGCTCATTTCAAAGGGAATACCTTTAGTCTTTCAGATTTCTGTCTTG 2140  
 Db 2247 AAGAACCAAAATTTGCTCATTTCAAAGGGAATACCTTTAGTCTTTCAGATTTCTGTCTTG 2306  
 QY 2141 ATATTCCTCCATTTCTGTGAGATTTAAACATTTCACTGTGCTGCAGGAAGTCCCGTCT 2200  
 Db 2307 ATATTCCTCCATTTCTGTGAGATTTAAACATTTCACTGTGCTGCAGGAAGTCCCGTCT 2366  
 QY 2201 CCGCGTGTGTCAGTAACCGGAGCCCTGCTGACCTGTGCTTCTCTCCCTGGAGGTTATA 2260  
 Db 2367 CCGCGTGTGTCAGTAACCGGAGCCCTGCTGACCTGTGCTTCTCTCCCTGGAGGTTATA 2426  
 QY 2261 CGCCACTACACCCAGCTGCTCTGCAAAATCTGCAATTCGGCAGCTCAAAAGGCATGAAC 2320  
 Db 2427 CGCCACTACACCCAGCTGCTCTGCAAAATCTGCAATTCGGCAGCTCAAAAGGCATGAAC 2486  
 QY 2321 AGATCTTCCAAAGTGCAGATCAATCTGAGAGTGAAACGAGAAACCATCTTCTTCTG 2380  
 Db 2487 AGATCTTCCAAAGTGCAGATCAATCTGAGAGTGAAACGAGAAACCATCTTCTTCTG 2546  
 QY 2381 CACAGAGGACAGACTTTCCTGCGACAGACTGCCCCCAAGCCTTCAAAATTCCTTACT 2440  
 Db 2547 CACAGAGGACAGACTTTCCTGCGACAGACTGCCCCCAAGCCTTCAAAATTCCTTACT 2606  
 QY 2441 CCATCAGACAGCGGATTTGTCTACATTTGATATCCCTCAATGCCAAGGCAAGGACTGGC 2500  
 Db 2607 CCATCAGACAGCGGATTTGTCTACATTTGATATCCCTCAATGCCAAGGCAAGGACTGGC 2666  
 QY 2501 AGATGTAGCACAGAAAAACAGCATCAACAGGAATTTATTTTCCTGCTACACAAGTA 2560  
 Db 2667 AGATGTAGCACAGAAAAACAGCATCAACAGGAATTTATTTTCCTGCTACACAAGTA 2726  
 QY 2561 GCCCATCTGCTGATTTTGAACCTGTGGAGTGGTCTCATCAGCATGATGGTGTCTTG 2620  
 Db 2727 GCCCATCTGCTGATTTTGAACCTGTGGAGTGGTCTCATCAGCATGATGGTGTCTTG 2786  
 QY 2621 ACTCCCTGGCTGTGCCCTTGAAGAGATTTGGGAGGACACACAGAACTCTCAAACTTT 2680  
 Db 2787 ACTCCCTGGCTGTGCCCTTGAAGAGATTTGGGAGGACACACAGAACTCTCAAACTTT 2846  
 QY 2681 CAGAACTCCAGCTGTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736  
 Db 2847 CAGAACTCCAGCTGTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2902

RESULT 9

ABX17909  
 ID ABX17909 standard; cDNA; 2979 BP.

XX AC ABX17909;

XX XX

XX 06-FEB-2003 (first entry)

XX cDNA encoding human G-protein coupled receptor GCRC-63.

XX Human; G-protein coupled receptor; GPCR; GCRC; INTSIG; cancer;

XX neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;

XX muscular disorder; myotonic dystrophy; catatonias; endocrine disorder;

XX diabetes; Grave's disease; leukaemia; cervical cancer; breast cancer;

XX immunological disorder; scleroderma; systemic lupus erythematosus;

XX allergy; gastrointestinal disorder; Crohn's disease; renal disorder;

XX Goodpasture's syndrome; infection; viral; bacterial; fungal; parasitic;

XX protozoal; helminthic; cardiovascular disorder; atherosclerosis;

XX hepatic disease; cirrhosis; transgenic; neuroprotective; relaxant;

XX antihypertensive; dermatological; immunosuppressive; uterine;

XX thyromimetic; antiinflammatory; cerebroprotective; gastrointestinal;

XX hepatotropic; nephrotropic; anticonvulsant; antirheumatic; cardiac;

XX nootropic; gene; ss.

OS Homo sapiens.  
 XX PN WO200279448-A2.  
 XX 10-OCT-2002.  
 XX PD 29-MAR-2002; 2002WO-US009923.  
 XX PP 30-MAR-2001; 2001US-0280683P.  
 XX PR 13-APR-2001; 2001US-0283714P.  
 XX PR 20-APR-2001; 2001US-0285336P.  
 XX PR 27-APR-2001; 2001US-0287266P.  
 XX PA (INCY-) INCYTE GENOMICS INC.  
 XX Thornton M, Yao MG, Richardson TW, Swarnakar A, Kallick DA;  
 PI Ison CH, Walia NK, Gandhi AR, Lee EA, Elliott VS, Hafalia AJA;  
 PI Au-Young J, Griffin JA, Baughn MR, Khan FA, Becha S, Lu Y;  
 PI Arvizu CP, Borowsky ML, Lal PG, Ramkumar J, Emerling BM, Walsh RT;  
 PI Yue H, Burford N, Graul RC;  
 XX WPI; 2003-058430/05.  
 DR P-PSDB; ABU11210.  
 XX PT New GCRC polypeptides, useful for diagnosing, preventing, and treating  
 PT disorders associated with an abnormal expression or activity of GCRC,  
 PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer and  
 PT infection.  
 XX Claim 5; Page 307-308; 313pp; English.  
 PS The present invention relates to the isolation of human G-protein coupled  
 XX receptors (GPCRs, designated GCRC), and the polynucleotide sequences  
 CC encoding them. The GCRC polypeptides or their fragments, and the  
 CC polynucleotide sequences encoding them are useful in diagnosing,  
 CC preventing, and treating disorders associated with an abnormal expression  
 CC or activity of INTSIG, such as neurodegenerative disorders (e.g. e.g.  
 CC Parkinson's disease, Alzheimer's disease), muscular disorders (e.g.  
 CC myotonic dystrophy, catatonias), endocrine disorders (e.g. diabetes,  
 CC Grave's disease), cancers (e.g. leukaemia, cervical or breast cancers),  
 CC immunological disorders (e.g. scleroderma, systemic lupus erythematosus,  
 CC allergies), gastrointestinal disorders (e.g. Crohn's disease), renal  
 CC disorders (e.g. Goodpasture's syndrome), infections (e.g. viral,  
 CC bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular  
 CC disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis).  
 CC GCRC or its fragments may also be used in screening for compounds that  
 CC specifically bind to and modulate the activity of GCRC. The  
 CC polynucleotides can be used to create humanised animals or transgenic  
 CC animals to model human disease. ABX17847-ABX17919 represent cDNA  
 CC sequences encoding the human GCRCs of the invention  
 XX  
 SQ Sequence 2979 BP; 764 A; 766 C; 740 G; 709 T; 0 U; 0 Other;  
 Query Match 83.6%; Score 2287; DB 10; Length 2979;  
 Best Local Similarity 91.3%; Pred. No. 0;  
 Matches 2560; Conservative 0; Mismatches 0; Indels 243; Gaps 3;  
 QY 102 AGGAAGTGAATGGGAGGAGCCCTTCCGAAATCCATCCATCCAGCTCTGGGACACTGCC 161  
 Db 213 AGGAAGTGAATGGGAGGAGCCCTTCCGAAATCCATCCATCCAGCTCTGGGACACTGCC 272  
 QY 162 TCATTTTCATAGAGGAGCCAGATGCTTATATATCAAGAGCAACCTTATGCACTCAG 221  
 Db 273 TCATTTTCATAGAGGAGCCAGATGCTTATATATCAAGAGCAACCTTATGCACTCAG 332  
 QY 222 GTCGAAGCGAGCCAGCCAGATGCTTATTTTCAATGCAAGCGGAGTGGTCCATCA 281  
 Db 333 GTCGAAGCGAGCCAGCCAGATGCTTATTTTCAATGCAAGCGGAGTGGTCCATCA 392  
 QY 282 GAACGAGCAGCTCTCTGAAGAGAGCTCTGGACGAGAGCTCAGGTTTGAAGTCCCGCAAGT 341  
 Db 393 GAACGAGCAGCTCTCTGAAGAGAGCTCTGGACGAGAGCTCAGGTTTGAAGTCCCGCAAGT 452

QY 342 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCATGGGCCCGAGGACTATTGGTG 401  
| | | | |  
Db 453 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCATGGGCCCGAGGACTATTGGTG 512  
| | | | |  
QY 402 CCAGTGTGGCGTGGAGCCACCTGGGTACCTCCAGAGCAGGAGGCGCTCTGTGGCAT 461  
| | | | |  
Db 513 CCAGTGTGGCGTGGAGCCACCTGGGTACCTCCAGAGCAGGAGGCGCTCTGTGGCAT 572  
| | | | |  
QY 462 AGCCTATTTACGGAAAACTTTGAACAAGACCACCAAGGAAGGAAGTTCCTCATTTGAAGG 521  
| | | | |  
Db 573 AGCCTATTTACGGAAAACTTTGAACAAGACCACCAAGGAAGGAAGTTCCTCATTTGAAGG 632  
| | | | |  
QY 522 CATGATTTGTAATGCACTGCCGCCACAGAGGAGTCCCTGCTGCCGAGGTGAATGGCT 581  
| | | | |  
Db 633 CATGATTTGTAATGCACTGCCGCCACAGAGGAGTCCCTGCTGCCGAGGTGAATGGCT 692  
| | | | |  
QY 582 GAAATATGAGAGCCCAATTGACTCTGAAACGAGACGAGAACATTTGACACCAAGGCGTACCA 641  
| | | | |  
Db 693 GAAATATGAGAGCCCAATTGACTCTGAAACGAGACGAGAACATTTGACACCAAGGCGTACCA 752  
| | | | |  
QY 642 TAACTCTGATCATCAGGAGGCAAGGCTCTCGGACTCAGGAAATTTACACCTGCAATGGCAGC 701  
| | | | |  
Db 753 TAACTCTGATCATCAGGAGGCAAGGCTCTCGGACTCAGGAAATTTACACCTGCAATGGCAGC 812  
| | | | |  
QY 702 CAACATCGTGGCTAAGAGGAGAAAGCCTGTCCGCCACTGTGTGGTCTTAC 750  
| | | | |  
Db 813 CAACATCGTGGCTAAGAGGAGAAAGCCTGTCCGCCACTGTGTGGTCTTACGTGAATGGAGG 872  
| | | | |  
QY 751 ----- 750  
| | | | |  
Db 873 CTGGTCTTCTGGAACAGAGTGGTCAGCCTGCAATGTCGATGTCGTTGGTAGAGATGGCAGAA 932  
| | | | |  
QY 751 ----- 750  
| | | | |  
Db 933 ACSTTCCGAGCCTGCACCAACCCAGCTCCTCTCAATGTGTGGGCGCTTTTGTGAGGGAAT 992  
| | | | |  
QY 751 ----- 773  
| | | | |  
Db 993 GTCAGTGCAGAAAAAATACCTGCACTTCTTTGTCCTGTGGATGGGAGCTGGGAAGTGTG 1052  
| | | | |  
QY 774 GAGGGAATGTCGTCTGAGTCCAGAGTGTGAACATTTCCGATCCGGAGTGCACAGC 833  
| | | | |  
Db 1053 GAGGGAATGTCGTCTGAGTCCAGAGTGTGAACATTTCCGATCCGGAGTGCACAGC 1112  
| | | | |  
QY 834 ACCACCCCGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCAGCAATCTCAAAACTG 893  
| | | | |  
Db 1113 ACCACCCCGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCAGCAATCTCAAAACTG 1172  
| | | | |  
QY 894 CACAGATGGCTTTGCACTCTAGATAAAAAAACCCTCTTCATGAAATAAAACCCCAAGCAT 953  
| | | | |  
Db 1173 CACAGATGGCTTTGCACTCTAG-----GCAT 1199  
| | | | |  
QY 954 TGGAATGCCAGCGACATTTGCTTTGTACTCGGCGTTGGGTGCTGCGGTGTGGCGCGTTGC 1013  
| | | | |  
Db 1200 TGGAATGCCAGCGACATTTGCTTTGTACTCGGCGTTGGGTGCTGCGGTGTGGCGCGTTGC 1259  
| | | | |  
QY 1014 AGTCTGGTCATTGGTGTCACTCTTACAGACGAGCCAGAGTGACTATGGCGTGCACGT 1073  
| | | | |  
Db 1260 AGTCTGGTCATTGGTGTCACTCTTACAGACGAGCCAGAGTGACTATGGCGTGCACGT 1319  
| | | | |  
QY 1074 CATTTGACTCTTCTGCAATGACAGGTGGCTTCCAGACTTCAACTTCAAAACAGTCCGTCA 1133  
| | | | |  
Db 1320 CATTTGACTCTTCTGCAATGACAGGTGGCTTCCAGACTTCAACTTCAAAACAGTCCGTCA 1379  
| | | | |  
QY 1134 AGCCAAGATATCATGGAATATGATACAGAAAAATCCTTTGGTTAACTCCCTGCTCCT 1193  
| | | | |  
Db 1380 A-----GGTAACCTCCCTGCTCCT 1397  
| | | | |  
QY 1194 GAATTTCTGCCATGCAGCCAGATCTGACAGTGAGCCGACATACAGCGGAGCCCATCTGTCT 1253  
| | | | |  
Db 1398 GAATTTCTGCCATGCAGCCAGATCTGACAGTGAGCCGACATACAGCGGAGCCCATCTGTCT 1457  
| | | | |  
QY 1254 GCAGGACCCCTCTGGCAAGAGGAGCTCATGACAGAGTCTCTCTTTAAACCTTTGTGCGA 1313  
| | | | |

Db 1458 GCAGGACCCCTCTGGCAAGAGGACTCATGACAGAGTCTCACTCTTTAAACCTTTGTGCGA 1517  
| | | | |  
QY 1314 CATCAAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTCTCTGAGAGAGCTGA 1373  
| | | | |  
Db 1518 CATCAAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTCTCTGAGAGAGCTGA 1577  
| | | | |  
QY 1374 GTACCAACGGCAAGATCATTTCCAGAGCTTTTCCCATGGAAAACAACACAGCTTTAGTAC 1433  
| | | | |  
Db 1578 GTACCAACGGCAAGATCATTTCCAGAGCTTTTCCCATGGAAAACAACACAGCTTTAGTAC 1637  
| | | | |  
QY 1434 AATGCATCCAGAAAATAAATGCTTACATCAAAAATCTGTCTCATCTCCTCCCAACAGGAC 1493  
| | | | |  
Db 1638 AATGCATCCAGAAAATAAATGCTTACATCAAAAATCTGTCTCATCTCCTCCCAACAGGAC 1697  
| | | | |  
QY 1494 AGNACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAATATC 1553  
| | | | |  
Db 1698 AGNACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAATATC 1757  
| | | | |  
QY 1554 AGGGGTGAGCTTACTCATACCAACCGGTGCCATCCAGAGGAGAAATTTCTGGGAGATTTA 1613  
| | | | |  
Db 1758 AGGGGTGAGCTTACTCATACCAACCGGTGCCATCCAGAGGAGAAATTTCTGGGAGATTTA 1817  
| | | | |  
QY 1614 TATGTCCATCAACCAAGGTGAACCCAGCTCCAGTCAGATGCTCTGAGGTGCTCCTGAG 1673  
| | | | |  
Db 1818 TATGTCCATCAACCAAGGTGAACCCAGCTCCAGTCAGATGCTCTGAGGTGCTCCTGAG 1877  
| | | | |  
QY 1674 TCTGTGAAGTCACTGTGGTCTCCAGACATGATCGTCAACCTCCCTTTGCAATGACCAT 1733  
| | | | |  
Db 1878 TCTGTGAAGTCACTGTGGTCTCCAGACATGATCGTCAACCTCCCTTTGCAATGACCAT 1937  
| | | | |  
QY 1734 CCGCAGCTGTGAGATGTCTGAGCAITTTGGAATATCCATTTAAAGAGAGGACACA 1793  
| | | | |  
Db 1938 CCGCAGCTGTGAGATGTCTGAGCAITTTGGAATATCCATTTAAAGAGAGGACACA 1997  
| | | | |  
QY 1794 GCAGGCAAAATGGGAGAAAGTGAATGTCTAGTGAAGATGAATCTACATCTCTGTTACTG 1853  
| | | | |  
Db 1998 GCAGGCAAAATGGGAGAAAGTGAATGTCTAGTGAAGATGAATCTACATCTCTGTTACTG 2057  
| | | | |  
QY 1854 TTTTGGACCCCTTTGGTGTCTATGTCCTCTGGAAGTCTTTGGAGCTATGCGCTCACTGG 1913  
| | | | |  
Db 2058 TTTTGGACCCCTTTGGTGTCTATGTCCTCTGGAAGTCTTTGGAGCTATGCGCTCACTGG 2117  
| | | | |  
QY 1914 AGAGCCAAATCACAGACTGTGCGGTGAAGCAACTGAAGTGTGGGCTTTTGGCTGCAATGC 1973  
| | | | |  
Db 2118 AGAGCCAAATCACAGACTGTGCGGTGAAGCAACTGAAGTGTGGGCTTTTGGCTGCAATGC 2177  
| | | | |  
QY 1974 CTGTAACTCCCTGGATTAACAATTGAGAGTTTACTGTGTGGAACAATAACCCCTTGTGCAT 2033  
| | | | |  
Db 2178 CTGTAACTCCCTGGATTAACAATTGAGAGTTTACTGTGTGGAACAATAACCCCTTGTGCAT 2237  
| | | | |  
QY 2034 TCAGGAGTGGTTTCAGATGAAGGCATCAAGGTGGACAGCTCTCGGAGAGCAAAAT 2093  
| | | | |  
Db 2238 TCAGGAGTGGTTTCAGATGAAGGCATCAAGGTGGACAGCTCTCGGAGAGCAAAAT 2297  
| | | | |  
QY 2094 GCTGCAITTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGCTTGAATATTTCCCCCAT 2153  
| | | | |  
Db 2298 GCTGCAITTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGCTTGAATATTTCCCCCAT 2357  
| | | | |  
QY 2154 CTTCTGGAGAAATAAACCAATCACTGCTGCGGAGAGTCCCGTTCCTCCCGGTGTGGTG 2213  
| | | | |  
Db 2358 CTTCTGGAGAAATAAACCAATCACTGCTGCGGAGAGTCCCGTTCCTCCCGGTGTGGTG 2417  
| | | | |  
QY 2214 CAGTAAACCGGACGCCCTGCACTGCTCTCCCTGGAGCGTTATACGCCCACTACCCAC 2273  
| | | | |  
Db 2418 CAGTAAACCGGACGCCCTGCACTGCTCTCCCTGGAGCGTTATACGCCCACTACCCAC 2477  
| | | | |  
QY 2274 CCAGTGTCTCTCAAAATCTGCAATTCGGCAGTCTCAAGAGCCCATGAACAGATCTCTCAAGT 2333  
| | | | |  
Db 2478 CCAGTGTCTCTCAAAATCTGCAATTCGGCAGTCTCAAGAGCCCATGAACAGATCTCTCAAGT 2537  
| | | | |  
QY 2334 GCAGACATCAATCTCTAGAGGTGAAGAGAAACCAATCACTTTCTTCTGCGACAGAGACAG 2393  
| | | | |

Db 2538 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCAAGAGGACAG 2597  
 Qy 2394 CACTTTCCCTGCGACAGACTGGCCGCCAAAGCCTTCAAAATTCCTACTCCATCAGACAGCG 2453  
 Db 2598 CACTTTCCCTGCGACAGACTGGCCGCCAAAGCCTTCAAAATTCCTACTCCATCAGACAGCG 2657  
 Qy 2454 GATTGTGCTACATTTGATACCCCTCCCAATGATGCAAGGCAAGGACTGGCAGATGTTAGCACA 2513  
 Db 2658 GATTGTGCTACATTTGATACCCCTCCCAATGATGCAAGGCAAGGACTGGCAGATGTTAGCACA 2717  
 Qy 2514 GAAAAACAGCATCAACAGAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCTGCTGT 2573  
 Db 2718 GAAAAACAGCATCAACAGAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCTGCTGT 2777  
 Qy 2574 CATTTTGAACCTGTGGAGCTGCTCATCAGCATGATGATGATCTTGAATCTCCCTGGCCTG 2633  
 Db 2778 CATTTTGAACCTGTGGAGCTGCTCATCAGCATGATGATGATCTTGAATCTCCCTGGCCTG 2837  
 Qy 2634 TGCCTTTGAAGAGATTGGGAGGACACACAGAACTCTCAAAATTTTCAAGATCCAGCT 2693  
 Db 2838 TGCCTTTGAAGAGATTGGGAGGACACACAGAACTCTCAAAATTTTCAAGATCCAGCT 2897  
 Qy 2694 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGAATCTAG 2736  
 Db 2898 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGAATCTAG 2940

RESULT 10

ADCT77423

ID ADC77423 standard; DNA; 2868 BP.

AC ADC77423;

XX

DT 01-JAN-2004 (first entry)

XX

DE Human transmembrane protein INSP017 full length cDNA sequence.

XX INSP017; transmembrane protein; netrin receptor family; netrin; axon;  
 KW cell migration; axon path-finding; central nervous system;  
 KW inflammatory disease; oncology; cardiovascular disease; cytoskeletal;  
 KW antiinflammatory; immunosuppressive; cardiant; anti-HIV; neuroprotective;  
 KW nootropic; antiparkinsonian; antidepressant; neuroleptic; osteopathic;  
 KW antiarteriosclerotic; nephrotropic; immunomodulator; antidiabetic;  
 KW antiinfertility; gene therapy; cell proliferative disorder;  
 KW myeloproliferative disorder; autoimmune disorder; inflammatory disorder;  
 KW cardiovascular disorder; neurological disorder; psychiatric disorder;  
 KW developmental disorder; bone disease; atherosclerosis;  
 KW glomerulonephritis; AIDS; HIV infection; metabolic disorder;  
 KW pregnancy disorder; birth complication; human; gene; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FH 1. .2868  
 FT /tag= a  
 FT /product= "Human INSP017 protein"  
 FT /partial  
 FT /note= "No stop codon"

XX WO2003055915-A2.

XX 10-JUL-2003.

XX 20-DEC-2002; 2002WO-GB005856.

XX 21-DEC-2001; 2001GB-00030721.

XX (ARES-) ARS TRADING SA.

XX Fitzgerald SN, Fagan RJ, Phelps CB, Power C, Yorke M;

XX WPI; 2003-559270/52.

XX P-PSDB; ADC77424.

DR

XX New polypeptide, useful for the manufacture of a medicament for treating  
 PT disease, e.g., cell proliferative, autoimmune, inflammatory,  
 PT cardiovascular or neurological disorders.  
 XX Claim 9; SEQ ID NO 33; 96pp; English.  
 XX This invention relates to a novel human protein (INSP017), a  
 CC transmembrane protein of the netrin receptor family, and to the use of  
 CC this protein and the DNA sequence which encodes it for diagnosis,  
 CC prevention and treatment of disease. Netrins are a family of secreted  
 CC proteins which are involved in both repelling and attracting axons and  
 CC thus function as guidance molecules for cell migration and axon path-  
 CC finding processes in the central nervous system. Transmembrane proteins  
 CC such as that of the invention have been shown to play a role in diverse  
 CC physiological functions and they may be involved in many diseases,  
 CC particularly inflammatory diseases, oncology and cardiovascular disease.  
 CC Compounds which modulate the transmembrane protein of the invention may  
 CC therefore have cytostatic, antiinflammatory, immunosuppressive, cardiant,  
 CC anti-HIV, neuroprotective, nootropic, antiparkinsonian, antidepressant,  
 CC immunomodulator, osteopathic, antiarteriosclerotic, nephrotropic,  
 CC neuroleptic, antidiabetic or antiinfertility activity. In addition,  
 CC the protein and amino acid sequence of the invention may be useful for  
 CC gene therapy. The protein, nucleic acid (and compound and pharmaceutical  
 CC composition) of the invention may be useful for the manufacture of a  
 CC medicament for treating disease, such as cell proliferative disorders,  
 CC myeloproliferative disorders, autoimmune/inflammatory disorders,  
 CC cardiovascular disorders, neurological disorders, psychiatric disorders,  
 CC developmental disorders, bone disease, atherosclerosis,  
 CC glomerulonephritis, AIDS, HIV infections, metabolic disorders, pregnancy  
 CC disorders and birth complications. The present sequence is the cloned  
 CC cDNA sequence which encodes the protein INSP017 of the invention.  
 XX  
 SQ Sequence 2868 BP; 732 A; 748 C; 714 G; 674 T; 0 U; 0 Other;  
 Query Match 83.5%; Score 2284; DB 10; Length 2868;  
 Best Local Similarity 91.3%; Pred. No. 0;  
 Matches 2557; Conservative 0; Mismatches 0; Indels 243; Gaps 3;  
 Qy 102 AGGAATCGAATGGCGAAGCCCTCCCGAATCCATCCATCAGCTCTGGGACACTGCC 161  
 Db 144 AGGAATCGAATGGCGAAGCCCTCCCGAATCCATCCATCAGCTCTGGGACACTGCC 203  
 Qy 162 TCATTTTCATAGAGGACCCAGATGATCTTATATATCAAGAGCAACCTATTGCATCAG 221  
 Db 204 TCATTTTCATAGAGGACCCAGATGATCTTATATATCAAGAGCAACCTATTGCATCAG 263  
 Qy 222 GTGCAAGCGAGCCAGCCATGCAGATATTCTTCAATGCAAGCGAGTGGGTCCATCA 281  
 Db 264 GTGCAAGCGAGCCAGCCATGCAGATATTCTTCAATGCAAGCGAGTGGGTCCATCA 323  
 Qy 282 GAACGAGCAGCTCTCTGAAGAGACTCTGGAAGAGAGCTCAGGTTTGAAGTCCGCGAAGT 341  
 Db 324 GAACGAGCAGCTCTCTGAAGAGACTCTGGAAGAGAGCTCAGGTTTGAAGTCCGCGAAGT 383  
 Qy 342 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGCCCGAGAGCTATTGGTG 401  
 Db 384 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGCCCGAGAGCTATTGGTG 443  
 Qy 402 CCAGTGTGTGGGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGCCCTCTGTGCGCAT 461  
 Db 444 CCAGTGTGTGGGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGCCCTCTGTGCGCAT 503  
 Qy 462 AGCCTATTTACGGAAAAAATCTTTGAAACAAGCCCAAGGAAGGAAAGTTCCTCATTTGAAGG 521  
 Db 504 AGCCTATTTACGGAAAAAATCTTTGAAACAAGCCCAAGGAAGGAAAGTTCCTCATTTGAAGG 563  
 Qy 522 CATGATGTGCTGCACTGGCCGCCACACAGGGAGTCCCTGTGCGAGAGTGAATGGCT 581  
 Db 564 CATGATGTGCTGCACTGGCCGCCCACACAGGGAGTCCCTGTGCGAGAGTGAATGGCT 623  
 Qy 582 GAAATATGAAGCCCATTTGACTCTGCAACAAGAGCAGGAACATTGACACACAGGCGCTGACCA 641



Db 624 GAAAAATGAAGACCCCACTGACTCTCTGAAACAGACGAGAAATGATGACACCCAGGCGCTGACCA 683  
Qy 642 TAACCTGATCATCAGGACGCGGCTCTCGACTCAGGAAATTAACCTGATGCGACG 701  
Db 684 TAACTGATCATCAGGACGCGGCTCTCGACTCAGGAAATTAACCTGATGCGACG 743  
Qy 702 CAACATCGTGGCTAAGAGAGAGAGCTGTGCGGCACTGTGTGGTCTAC 750  
Db 744 CAACATCGTGGCTAAGAGAGAGAGCTGTGCGGCACTGTGTGGTCTAAGTGAAGG 803  
Qy 751 ----- 750  
Db 804 CTGGTCTTCTCTGGAACAGAGTGGTGCAGCTGCAATGTTGCTGTGGTGTAGAGATGGCAGAA 863  
Qy 751 ----- 750  
Db 864 ACCTTCCCGACCTGCACCAACCCAGCTCCTCTCAATGTTGGGCTTTTGTGAGGGAAT 923  
Qy 751 ----- GTGGATGGGAGCTGGGAAGTGTG 773  
Db 924 GTCAGTGCAGAAATAACCTGCACTTCTTTGTCTGTGGATGGAGCTGGGAGTGTG 983  
Qy 774 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGC 833  
Db 984 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGC 1043  
Qy 834 ACCACCCCGAGAAATGGGGGCAAAATCTCTGAAGGTCTAAGCCAGGAATCTGAACCTG 893  
Db 1044 ACCACCCCGAGAAATGGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAATCTGAACCTG 1103  
Qy 894 CACAGATGGTCTTTGATCCTAGATAAAACCTTCTCATGAATAAAACCCCAAGCAT 953  
Db 1104 CACAGATGGTCTTTGATCCTAG -----GCAT 1130  
Qy 954 TGAAGATGCCAGCGAACATTTGCTTTTGTATCTCGGCTTGGGTGTGCTGCGCTGCGCTTGC 1013  
Db 1131 TGAAGATGCCAGCGAACATTTGCTTTTGTATCTCGGCTTGGGTGTGCTGCGCTGCGCTTGC 1190  
Qy 1014 AGTCCTGTGCTATGTTGTGTCACCTTTTACAGCGGAGCCAGAGTACATATGGGTGACCT 1073  
Db 1191 AGTCCTGTGCTATGTTGTGTCACCTTTTACAGCGGAGCCAGAGTACATATGGGTGACCT 1250  
Qy 1074 CATTTGACTCTTTGCTGATGACAGGTGGCTTCCAGAGCTTCAACTTCAAAACAGTCCGTCA 1133  
Db 1251 CATTTGACTCTTTGCTGATGACAGGTGGCTTCCAGAGCTTCAACTTCAAAACAGTCCGTCA 1310  
Qy 1134 AGCCAAGATATCATGGAATATGATACAGAAAAATCCTTTGGTAACTCCCTGCTCCT 1193  
Db 1311 A-----GGTAACTCCCTGCTCCT 1328  
Qy 1194 GAATTCCTGCATGCAGCCAGATCTGACAGTGGAGCCGGAATACAGCGGACCCCATCTGTCT 1253  
Db 1329 GAATTCCTGCATGCAGCCAGATCTGACAGTGGAGCCGGAATACAGCGGACCCCATCTGTCT 1388  
Qy 1254 GCAGGACCTCTGGAACAAGGAGCTCATGACAGAGTCTCTCACTTTTAAACCTTTGTGCGA 1313  
Db 1389 GCAGGACCTCTGGAACAAGGAGCTCATGACAGAGTCTCTCACTTTTAAACCTTTGTGCGA 1448  
Qy 1314 CATCAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTCTGAGAGAGCTGA 1373  
Db 1449 CATCAAGTGAAGTCCAGAGCTCGTTTCATGTTTCCCTGGGAGTCTGAGAGAGCTGA 1508  
Qy 1374 GTACCAAGGCAAGAAATCATTCAGGACTTTTCCCATGGAACCAACACAGCTTTTAGTAC 1433  
Db 1509 GTACCAAGGCAAGAAATCATTCAGGACTTTTCCCATGGAACCAACAGCTTTTAGTAC 1568  
Qy 1434 AATGCATCCAGAAATAAAATGCCCTATCATCCAAATCTGTCTATCATCTCCCAACAAGGAC 1493  
Db 1569 AATGCATCCAGAAATAAAATGCCCTATCATCCAAATCTGTCTATCATCTCCCAACAAGGAC 1628  
Qy 1494 AGAATCTGAGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAATATAC 1553  
Db 1629 AGAATCTGAGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAATATAC 1688

Qy 1554 AGGGGTGAGCTTACTCATACACACGGTGCATCCAGAGGAGAAATTTCTTGGGAGATTTA 1613  
Db 1689 AGGGGTGAGCTTACTCATACACACGGTGCATCCAGAGGAGAAATTTCTTGGGAGATTTA 1748  
Qy 1614 TATGTCCATCAACCAAGGTGAACCCAGGCTCCAGTCAGATGGCTCTGAGGTCTCTGAG 1673  
Db 1749 TATGTCCATCAACCAAGGTGAACCCAGGCTCCAGTCAGATGGCTCTGAGGTCTCTGAG 1808  
Qy 1674 TCTGAAAGTCACTGTGTCTCCAGACATGATCGTCAACCTCCCTTTGCAATGACCAT 1733  
Db 1809 TCTGAAAGTCACTGTGTCTCCAGACATGATCGTCAACCTCCCTTTGCAATGACCAT 1868  
Qy 1734 CCGCAGCTGTGCAGATGTCTGAGCATTTGGAATATCCATTTAAAGAAAGAGACACA 1793  
Db 1869 CCGCAGCTGTGCAGATGTCTGAGCATTTGGAATATCCATTTAAAGAAAGAGACACA 1928  
Qy 1794 GCAGGGCAAAATGGGAGGAAGTGTGATGTGAGTGAAGATGAATCTATCTCTGTATGCTC 1853  
Db 1929 GCAGGGCAAAATGGGAGGAAGTGTGATGTGAGTGAAGATGAATCTATCTCTGTATGCTC 1988  
Qy 1854 TTTGGAACCTTTTGGTGTCTCTCTGACAGCTTTTGGGACCTATGCCCTCACTCG 1913  
Db 1989 TTTGGAACCTTTTGGTGTCTCTCTGACAGCTTTTGGGACCTATGCCCTCACTCG 2048  
Qy 1914 AGAGCCAAATCAAGAGCTGTGCGGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGATGTC 1973  
Db 2049 AGAGCCAAATCAAGAGCTGTGCGGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGATGTC 2108  
Qy 1974 CTGTAACTCCCTGGATTAACAATTGAGAGTTTACTGTGTGAGCAATACCCCTTTGTGCA 2033  
Db 2109 CTGTAACTCCCTGGATTAACAATTGAGAGTTTACTGTGTGAGCAATACCCCTTTGTGCA 2168  
Qy 2034 TCAGGAAGTGGTTTCAGATGAAGGCATCAAGTGGAGAGCTTCTGGAGAGACCAAAAT 2093  
Db 2169 TCAGGAAGTGGTTTCAGATGAAGGCATCAAGTGGAGAGCTTCTGGAGAGACCAAAAT 2228  
Qy 2094 GCTGTAACTTCAAGGGGAATACCTTTAGTCTTCAGATTTCTGTCTCTGTATTTCCCCCA 2153  
Db 2229 GCTGTAACTTCAAGGGGAATACCTTTAGTCTTCAGATTTCTGTCTCTGTATTTCCCCCA 2288  
Qy 2154 CTTCTGGAGAAATTAACAATTCACTGCTGCCAGGAAGTCCCGTTCTCCCGGTGTGGTG 2213  
Db 2289 CTTCTGGAGAAATTAACAATTCACTGCTGCCAGGAAGTCCCGTTCTCCCGGTGTGGTG 2348  
Qy 2214 CAGTAACCGGACGCGCTGCACTGTGCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2273  
Db 2349 CAGTAACCGGACGCGCTGCACTGTGCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2408  
Qy 2274 CCAGCTGTCTCGCAAAATCTGCAATTCGGCAGCTCAAGGCCATGAACAGATCTCCAAGT 2333  
Db 2409 CCAGCTGTCTCGCAAAATCTGCAATTCGGCAGCTCAAGGCCATGAACAGATCTCCAAGT 2468  
Qy 2334 GCAGACATCAATCTTAGAGAGTGAAGAGAAACCATCACTTTCTGCAAGAGAGACAG 2393  
Db 2469 GCAGACATCAATCTTAGAGAGTGAAGAGAAACCATCACTTTCTGCAAGAGAGACAG 2528  
Qy 2394 CACTTTCCCTGACAGAGCTGGCCCAAGCCCTTAAATTCCTACTCTCATCAGACAGCG 2453  
Db 2529 CACTTTCCCTGACAGAGCTGGCCCAAGCCCTTAAATTCCTACTCTCATCAGACAGCG 2588  
Qy 2454 GATTTGTGTACATTTGTATACCCCAATGCCAAAGGCAAGGATGGCAGATGTTAGCA 2513  
Db 2589 GATTTGTGTACATTTGTATACCCCAATGCCAAAGGCAAGGATGGCAGATGTTAGCA 2648  
Qy 2514 GAAACACAGCATCAACAGGAATTTATCTTATTTCTGCTACAAAGTAGCCCATCTGCTGT 2573  
Db 2649 GAAACACAGCATCAACAGGAATTTATCTTATTTCTGCTACAAAGTAGCCCATCTGCTGT 2708  
Qy 2574 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGTTGATCTTTGACTCCCTGCGCTG 2633  
Db 2709 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGTTGATCTTTGACTCCCTGCGCTG 2768





Db 638 TAACCTCATCATCAGGAGGCAAGGCTCTCGGACTCAGGAAATTTACACCTGCATGGCAGC 697  
QY 702 CAACATCGTGGCTTAAGAGGAGAGCCCTGTGGCCACCTGTGGTCTAC-----750  
Db 698 CAACATCGTGGCTTAAGAGGAGAGCCCTGTGGCCACCTGTGGTCTACGTGAATGGAGG 757  
QY 751 -----750  
Db 758 CTGCTCTTCTGGACAGAGTGGTCAGCCTGCAATGTTGCTGTCGTGTAGAGATGGCAGAA 817  
QY 751 -----750  
Db 818 ACGTTCCGGACCTGCACCAACCAGCTCCTCTCAATGTGGGGCCCTTTTGTGAGGGAAT 877  
QY 751 -----GTGGATGGGAGCTGGGAAGTGTG 773  
Db 878 GTGAGTCAGAAATAAACCTGCACTTCTTTGTCTGTGGATGGGAGCTGGGAAGTGTG 937  
QY 774 GAGCGAATGCTCGGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGC 833  
Db 938 GAGCGAATGCTCGGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGAGTGCACAGC 997  
QY 834 ACCACCCCGAGAAATGGGGGCAAAATTTCTGTGAAGGTCTAAGCCAGGAATCTGAATACTG 893  
Db 998 ACCACCCCGAGAAATGGGGGCAAAATTTCTGTGAAGGTCTAAGCCAGGAATCTGAATACTG 1057  
QY 894 CACAGATGCTTTGTGATCTCTAGATAAAACCTCTTCAATAAATAAAACCCCAAGC-- 951  
Db 1058 CACAGATGCTTTGTGATCTCTAGATAAAACCTCTTCAATAAATAAAACCCCAAGC-- 1117  
QY 952 -----ATTGAGAATCCAGCGACATTTGCTGTGCTCTCGGGCTTGGGTGC 995  
Db 1118 TCAGACGCTATGCCAAATTCAGAAATCCAGCGACATTTGCTGTGCTCTCGGGCTTGGGTGC 1177  
QY 996 TGGCGTGTGGCGTGTGAGTCTCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1055  
Db 1178 TGGCGTGTGGCGTGTGAGTCTCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1237  
QY 1056 TGACTATGGCGTGGAGTCTGATCTGCTGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1115  
Db 1238 TGACTATGGCGTGGAGTCTGATCTGCTGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1297  
QY 1116 CTTTCAAAACAGTCCGTCAGCCAGCAAGAAATATCATGGAACCTAAATGATCAAGAAATCTCTT 1175  
Db 1298 CTTTCAAAACAGTCCGTCAGCA-----1316  
QY 1176 TGCTAACTCCCTGCTCTGAAATTTCTGCCATGCGCAGATCTGACAGTGAAGCCGAGATA 1235  
Db 1317 -GGGAACTCCCTGCTCTGAAATTTCTGCCATGCGCAGATCTGACAGTGAAGCCGAGATA 1375  
QY 1236 CAGCGGACCATCTGTCTGAGGACCTCTGGCAAGGAGCTCATGACAGAGTCTCTCACT 1295  
Db 1376 CAGCGGACCATCTGTCTGAGGACCTCTGGCAAGGAGCTCATGACAGAGTCTCTCACT 1435  
QY 1296 CTTTAAACCTTTGTCCGACATCAAGGTGAAGTCCAGAGTCTGTTTCAATGTTTCCCTGGG 1355  
Db 1436 CTTTAAACCTTTGTCCGACATCAAGGTGAAGTCCAGAGTCTGTTTCAATGTTTCCCTGGG 1495  
QY 1356 AGTGTCTGAGAGCTGAGTACACCGCAAGATCAATTCAGGACTTTTCCCATCGAAA 1415  
Db 1496 AGTGTCTGAGAGCTGAGTACACCGCAAGATCAATTCAGGACTTTTCCCATCGAAA 1555  
QY 1416 CAACACAGCTTTAGTACAAATGATCCAGAAATAAATGTCCTTACATCCAAATCTGTC 1475  
Db 1556 CAACACAGCTTTAGTACAAATGATCCAGAAATAAATGTCCTTACATCCAAATCTGTC 1615  
QY 1476 ATCACTCCCAAGGACAGAACTGAGCAAACTGGTGTCTTTGGCCATTTAGGGGGGG 1535  
Db 1616 ATCACTCCCAAGGACAGAACTGAGCAAACTGGTGTCTTTGGCCATTTAGGGGGGG 1675  
QY 1536 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTATACCAACAGCGTGCATCCACAGGA 1595

Db 1676 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTATACCAACACGTCCTATCCACAGGA 1735  
QY 1596 GAATTCCTGGAGATTTATATGTCATCAACCAAGGTGAACCCAGCTCCAGTCCAGATGG 1655  
Db 1736 GAATTCCTGGAGATTTATATGTCATCAACCAAGGTGAACCCAG-----GTCAGATGG 1789  
QY 1656 CTTCTGAGGTGCTCCTCAGTCTCAAGTCACTGTGCTCTCCAGACATGATCTGACCAC 1715  
Db 1790 CTTCTGAGGTGCTCCTCAGTCTCAAGTCACTGTGCTCTCCAGACATGATCTGACCAC 1849  
QY 1716 TCCCTTTGATTTGACCAATCCCGACCTGTGAGATGTCAGTCTGAGATTTGGAATATCCA 1775  
Db 1850 TCCCTTTGATTTGACCAATCCCGACCTGTGAGATGTCAGTCTGAGATTTGGAATATCCA 1909  
QY 1776 TTTAAAGAGAGACACAGCAGGGCAAAATGGGAGGAAGTGAATGTCAGTGAAGATGAATC 1835  
Db 1910 TTTAAAGAGAGACACAGCAGGGCAAAATGGGAGGAAGTGAATGTCAGTGAAGATGAATC 1869  
QY 1836 TACATCCTGTTACTGCTTTTGGACCCCTTTTGGCTGTCATGTCCTCTGACAGCTTTTGG 1895  
Db 1970 TACATCCTGTTACTGCTTTTGGACCCCTTTTGGCTGTCATGTCCTCTGACAGCTTTTGG 2029  
QY 1896 GACCTATGCGCTCACTGGAGAGCCAAATCAAGCTGTGCGGTGAAGAGTGGC 1955  
Db 2030 GACCTATGCGCTCACTGGAGAGCCAAATCAAGCTGTGCGGTGAAGAGTGGC 2089  
QY 1956 GGTTTTGGCTGATGCTGCTGTAACCTCCCTGGATTAACAATTTGAGAGTTTACTGTGTGGA 2015  
Db 2090 GGTTTTGGCTGATGCTGCTGTAACCTCCCTGGATTAACAATTTGAGAGTTTACTGTGTGGA 2149  
QY 2016 CAATACCCCTTGTGCAATTTCAGGAAGTGGTTTTCAGATGAAGGCATCAAGGTGGACAGCT 2075  
Db 2150 CAATACCCCTTGTGCAATTTCAGGAAGTGGTTTTCAGATGAAGGCATCAAGGTGGACAGCT 2209  
QY 2076 CTTGGAAGAACCAAAATTTGCTGCAATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2135  
Db 2210 CTTGGAAGAACCAAAATTTGCTGCAATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2269  
QY 2136 CTTTGTATTTTCCCCCATCTCTGGAGAAATTAACCATTTCACTGCTGCCAGGAAGTCCC 2195  
Db 2270 CTTTGTATTTTCCCCCATCTCTGGAGAAATTAACCATTTCACTGCTGCCAGGAAGTCCC 2329  
QY 2196 GTTCTCCCGTGTGTGTCAGTAACCGGACGCCCCCTGCACTGTGCTTCTCCTGTGAGCG 2255  
Db 2330 GTTCTCCCGTGTGTGTCAGTAACCGGACGCCCCCTGCACTGTGCTTCTCCTGTGAGCG 2389  
QY 2256 TTATAGCCCCCATACACACCGAGTGTCTGCAAAATCTGCAATTCGCGAGCTCAAGGCGCA 2315  
Db 2390 TTATAGCCCCCATACACACCGAGTGTCTGCAAAATCTGCAATTCGCGAGCTCAAGGCGCA 2449  
QY 2316 TGAACAGATCTCTCAAGTCAGACATCAATCTAGAGAGTGAACAGGAACCAATCACTTT 2375  
Db 2450 TGAACAGATCTCTCAAGTCAGACATCAATCTAGAGAGTGAACAGGAACCAATCACTTT 2509  
QY 2376 CTTTGCACAAGAGGACAGCACTTTTCCCTGACAGACTGGCCCCCAAGCCCTTCAAAATTC 2435  
Db 2510 CTTTGCACAAGAGGACAGCACTTTTCCCTGACAGACTGGCCCCCAAGCCCTTCAAAATTC 2569  
QY 2436 CTACTCCATCAGACAGCGAATTTGTGCTACATTTGATATCCCCCAATGCCAAGGCGAAGGA 2495  
Db 2570 CTACTCCATCAGACAGCGAATTTGTGCTACATTTGATATCCCCCAATGCCAAGGCGAAGGA 2629  
QY 2496 CTGGCAGATGTTAGCACAGAAAAACAGCATCAAC--AGGAATTTATCTTATTTCCCTAC 2552  
Db 2630 CTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAGGAATTTATCTTATTTCCCTAC 2689  
QY 2553 ACAAGATAGCCCATCTGCTGTCATTTTGAACTGTGGGAAGCTGTCATCAGCATGATGG 2612  
Db 2690 ACAAGATAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTGTCATCAGCATGATGG 2749  
QY 2613 TGAATCTTGACTCCCTGGCGCTGTGCTTGAAGAGATTTGGAGGACACACAGGAACCTCTC 2672  
Db 2750 TGAATCTTGACTCCCTGGCGCTGTGCTTGAAGAGATTTGGAGGACACACAGGAACCTCTC 2809

QY 2673 AACATTTCAGATCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGCACT 2732  
 |||||  
 Db 2810 AACATTTCAGATCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGCACT 2869  
 |||||  
 QY 2733 CTAG 2736  
 |||||  
 Db 2870 CTAG 2873  
 |||||  
 RESULT 12  
 ADL24070  
 ID ADL24070 standard; cDNA; 2898 BP.  
 XX  
 AC ADL24070;  
 XX  
 XX 20-MAY-2004 (first entry)  
 XX  
 DE Human NOVX cDNA #58.  
 XX  
 KW Human; NOVX; gene; ss; G protein-coupled receptor; GPCR; cardiomyopathy;  
 KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;  
 KW atrial septal defect; ASD; atrioventricular canal defect;  
 KW ductus arteriosus; pulmonary stenosis; subaortic stenosis;  
 KW ventricular septal defect; VSD; tuberculous sclerosis; scleroderma; obesity;  
 KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;  
 KW neoplasm; adenocarcinoma; lymphoma; uterine cancer; haemophilia;  
 KW hypercoagulability; idiopathic thrombocytopenia purpura;  
 KW immunodeficiency; graft-versus-host disease; AIDS; bronchial asthma;  
 KW Crohn's disease; multiple sclerosis;  
 KW Albright's hereditary osteodystrophy; diabetes; infectious diseases;  
 KW anorexia; neurodegenerative disorder; Alzheimer's disease;  
 KW Parkinson's disease; haematopoietic disorder; metabolic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004002120-A1.  
 XX  
 XX 01-JAN-2004.  
 XX  
 PD 07-MAR-2002; 2002US-00094886.  
 PF  
 XX 08-MAR-2001; 2001US-0274194P.  
 PR 08-MAR-2001; 2001US-0274281P.  
 PR 08-MAR-2001; 2001US-0274322P.  
 PR 09-MAR-2001; 2001US-0274849P.  
 PR 12-MAR-2001; 2001US-0275235P.  
 PR 13-MAR-2001; 2001US-0275578P.  
 PR 13-MAR-2001; 2001US-0275579P.  
 PR 13-MAR-2001; 2001US-0275601P.  
 PR 14-MAR-2001; 2001US-0276000P.  
 PR 16-MAR-2001; 2001US-0276776P.  
 PR 19-MAR-2001; 2001US-0276994P.  
 PR 20-MAR-2001; 2001US-0277239P.  
 PR 20-MAR-2001; 2001US-0277327P.  
 PR 20-MAR-2001; 2001US-0277388P.  
 PR 21-MAR-2001; 2001US-0277791P.  
 PR 22-MAR-2001; 2001US-0277833P.  
 PR 23-MAR-2001; 2001US-0278152P.  
 PR 26-MAR-2001; 2001US-0278894P.  
 PR 27-MAR-2001; 2001US-0278999P.  
 PR 27-MAR-2001; 2001US-0279036P.  
 PR 30-MAR-2001; 2001US-0280233P.  
 PR 02-APR-2001; 2001US-0280802P.  
 PR 02-MAY-2001; 2001US-0280852P.  
 PR 02-MAY-2001; 2001US-0288066P.  
 PR 02-MAY-2001; 2001US-0288228P.  
 PR 17-MAY-2001; 2001US-0291766P.  
 PR 07-JUN-2001; 2001US-0296693P.  
 PR 08-JUN-2001; 2001US-0296856P.  
 PR 05-JUL-2001; 2001US-0303230P.  
 PR 05-JUL-2001; 2001US-0303237P.  
 PR 08-AUG-2001; 2001US-0310913P.  
 PR 13-AUG-2001; 2001US-0311978P.  
 PR 14-AUG-2001; 2001US-0312191P.  
 PR 16-AUG-2001; 2001US-0312916P.  
 PR 17-AUG-2001; 2001US-0313182P.  
 PR 20-AUG-2001; 2001US-0313626P.  
 PR 21-AUG-2001; 2001US-0314018P.  
 PR 27-AUG-2001; 2001US-0315227P.  
 PR 10-SEP-2001; 2001US-0318403P.  
 PR 14-SEP-2001; 2001US-0318510P.  
 PR 14-SEP-2001; 2001US-0322360P.  
 PR 27-SEP-2001; 2001US-0325378P.  
 PR 09-NOV-2001; 2001US-0332486P.  
 PR 09-NOV-2001; 2001US-0345399P.  
 XX  
 PA (KEKU/) KEKUDA R.  
 PA (TCHE/) TCHERNEV V T.  
 PA (LIUX/) LIU X.  
 PA (SPYT/) SPYTEK K A.  
 PA (PATT/) PATTURAJAN M.  
 PA (BURG/) BURGESS C E.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (MALI/) MALYANKAR U M.  
 PA (BOLD/) BOLDG F L.  
 PA (GUOX/) GUO X.  
 PA (SHEN/) SHENOY S G.  
 PA (PADI/) PADIGARU M.  
 PA (TAUP/) TAUPIER R J.  
 PA (MILL/) MILLER C E.  
 PA (CASW/) CASMAN S J.  
 PA (PENA/) PENNA C E A.  
 PA (GANG/) GANGOLLI E A.  
 PA (GUSE/) GUSEV V Y.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (GERL/) GERLACH V.  
 PA (POCH/) POCHART P F.  
 PA (FERN/) FERNANDES E R.  
 PA (SHIM/) SHIMKETS R A.  
 PA (RASI/) RASTELLI L.  
 PA (SPAD/) SPADERNA S K.  
 PA (LARO/) LAROCHELLE W J.  
 PA (ZHON/) ZHONG M.  
 PA (KHRA/) KHRAMTSOV N V.  
 PA (VOSS/) VOSS E Z.  
 PA (HERR/) HERRMANN J L.  
 XX  
 PI Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M;  
 PI Burgess CE, Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL;  
 PI Guo X, Shenoy SG, Padigar M, Taupier RJ, Miller CE, Casman SJ;  
 PI Pena CE, Gangolli EA, Gusev VY, Smithson G, Zerhusen BD, Gerlach V;  
 PI Pochart PF, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK;  
 PI Larochelle WJ, Zhong M, Khrantsov NV, Voss EZ, Herrmann JL;  
 WPI; 2004-212692/20.  
 DR P-PSDB; ADL24071.  
 DR  
 XX  
 PT Novel isolated G protein-coupled receptor polypeptides, referred as NOVX,  
 PT useful for treating scleroderma, obesity, congenital adrenal hyperplasia,  
 PT prostate cancer, hemophilia, AIDS, bronchial asthma, Crohn's disease.  
 XX  
 PS Claim 23; SEQ ID NO 115; 287pp; English.  
 XX  
 CC The invention relates to human G protein-coupled receptor-related (GPCR-  
 CC related) polypeptides (designated NOVX) and the polynucleotides encoding  
 CC them. The polypeptides and polynucleotides are useful as therapeutics in  
 CC the manufacture of medicaments for treating syndromes associated with  
 CC human diseases. The sequences are useful for treating a disorder  
 CC associated with aberrant NOVX expression or activity such as  
 CC cardiomyopathy, atherosclerosis, hypertension, congenital heart defects,  
 CC aortic stenosis, atrial septal defect (ASD), atrioventricular canal

CC defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis,  
 CC ventricular septal defect (VSD), tuberculous sclerosis, scleroderma,  
 CC obesity, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate  
 CC cancer, neoplasm, adenocarcinoma, lymphoma, uterine cancer, haemophilia,  
 CC hypercoagulability, idiopathic thrombocytopenia purpura,  
 CC immunodeficiencies, graft-versus-host disease, AIDS, bronchial asthma,  
 CC Crohn's disease, multiple sclerosis, Albrecht's hereditary  
 CC osteodysrophy, diabetes, infectious diseases, anorexia,  
 CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,  
 CC immune disorders, haematopoietic disorders and metabolic disorders. This  
 CC sequence represents human NOVX cDNA of the invention.  
 XX  
 SQ Sequence 2898 BP; 750 A; 760 C; 725 G; 663 T; 0 U; 0 Other;

Query Match 82.6%; Score 2260; DB 12; Length 2898;  
 Best Local Similarity 90.7%; Pred. No. 0;  
 Matches 2562; Conservative 0; Mismatches 25; Indels 237; Gaps 5;

QY 102 AGGAACGTGACATGGCGAGCCCTTCCGGAATCCATCCCATGAGCTCTGGGACACTGCC 161  
 DB 98 AGGAACGTGACATGGCGAGCCCTTCCGGAATCCATCCCATGAGCTCTGGGACACTGCC 157  
 QY 162 TCATTTTCATAGAGGAGCCAGATGATCTTATATATCAAGAGCAACCTATTGCACTCAG 221  
 DB 158 TCATTTTCATAGAGGAGCCAGATGATCTTATATATCAAGAGCAACCTATTGCACTCAG 217  
 QY 222 GTCCAAAGCGAGCCAGCCATGAGATATTTCTTCAATGCAACGGCGAGTGGTCCATCA 281  
 DB 218 GTCCAAAGCGAGCCAGCCATGAGATATTTCTTCAATGCAACGGCGAGTGGTCCATCA 277  
 QY 282 GAACGAGCAGCTCTGAGAGAGACTCTGGACGAGCTCAGGTTGAAGTCCGCAAGT 341  
 DB 278 GAACGAGCAGCTCTGAGAGAGACTCTGGACGAGCTCAGGTTGAAGTCCGCAAGT 337  
 QY 342 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGCCCGAGGACTATTGGTG 401  
 DB 338 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGCCCGAGGACTATTGGTG 397  
 QY 402 CCAGTGTGTGGCGTGGAGCCACTGGGTACTCTCAAGAGAGAGGAGCCCTCTGTGGCGAT 461  
 DB 398 CCAGTGTGTGGCGTGGAGCCACTGGGTACTCTCAAGAGAGAGGAGCCCTCTGTGGCGAT 457  
 QY 462 AGCCTATTTACGAAAAAATTGAAACAGACCACCAAGAGAGGAGGATTTCCCATTTGAAG 521  
 DB 458 AGCCTATTTACGAAAAAATTGAAACAGACCACCAAGAGAGGAGGATTTCCCATTTGAAG 517  
 QY 522 CATGATTGTACTGCACCTCGCCGCCACACAGAGGAGTCCCTGCTCGCGAGTGGATGGCT 581  
 DB 518 CATGATTGTACTGCACCTCGCCGCCACACAGAGGAGTCCCTGCTCGCGAGTGGATGGCT 577  
 QY 582 GAAAAATGAAGAGCCCATTTGACTCTGAACAGAGAGAGAACTTGAACAGAGGAGGCTGACCA 641  
 DB 578 GAAAAATGAAGAGCCCATTTGACTCTGAACAGAGAGAGAACTTGAACAGAGGAGGCTGACCA 637  
 QY 642 TAACCTGATCATAGGAGGAGCGGCTCTGGACTCAGGAAATTACACCTGCATGGCAGC 701  
 DB 638 TAACTCTGATCATAGGAGGAGCGGCTCTGGACTCAGGAAATTACACCTGCATGGCAGC 697  
 QY 702 CAACATCTGGTGAAGAGGAGAGCTGTGCGGCCACTGTTGGTGTCTAC----- 750  
 DB 698 CAACATCTGGTGAAGAGGAGAGCTGTGCGGCCACTGTTGGTGTCTACGTGAATGGAGG 757  
 QY 751 ----- 750  
 DB 758 CTGGTCTTCTCGACAGAGTGGTTCAGCTGCAATGTTTCGCTGTGGTAGAGGATGGCAGAA 817  
 QY 751 ----- 750  
 DB 818 ACCTTCCCGAGCCTGCACCAACCCAGCTCCTCTCAATGGTGGGCGCTTTTGTGAGGGAAT 877  
 QY 751 -----GTGGATGGGAGCTGGGAAGTGTG 773  
 DB 878 GTCAGTGCAGAAATAACCTGCACCTTCTTTGCTCTGTGGATGGGAGCTGGGAAGTGTG 937

QY 774 GAGCGAATGGTCCGCTCGAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 833  
 DB 938 GAGCGAATGGTCCGCTCGAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 997  
 QY 834 ACCACCCCGAGAAATGGGGGCAAAATCTGCTAGGCTCTAAGCCAGGAATCTTGAAACATG 893  
 DB 998 ACCACCCCGAGAAATGGGGGCAAAATCTGCTAGGCTCTAAGCCAGGAATCTTGAAACATG 1057  
 QY 894 CACAGATGTCTTTGTCATCCTTAGATAAAAAAACCCTTTCATGAATAAAAAACCCCAAGC-- 951  
 DB 1058 CACAGATGTCTTTGTCATCCTTAACTCCACCAACCATGACAGGAACCCCAAGTGAATCTT 1117  
 QY 952 -----ATTGAAATGCCAGCGACATGCTTTGTACTCGGGCTTGGGTGC 995  
 DB 1118 TCAGACGCTATGCCAAATTTGAGAAATGCCAGCGACATGCTTTGTACTCGGGCTTGGGTGC 1177  
 QY 996 TGCCTGCTGGCGGTTGAGTCTCTGTCATGCTGCTGTCACCTTTACAGACGGAGCCAGAG 1055  
 DB 1178 TGCCTGCTGGCGGTTGAGTCTCTGTCATGCTGCTGTCACCTTTACAGACGGAGCCAGAG 1237  
 QY 1056 TGAATATGGCGTGGAGCTCATTTGACTCTTCTGCAATGACAGGTGGTTCAGACCTTCAA 1115  
 DB 1238 TGAATATGGCGTGGAGCTCATTTGACTCTTCTGCAATGACAGGTGGTTCAGACCTTCAA 1297  
 QY 1116 CTTCAAAACAGTCCGTCAGCCAAAGATATCATGGAATTAATGATACAAAGAAATTCCTT 1175  
 DB 1298 CTTCAAAACAGTCCGTCMA----- 1316  
 QY 1176 TGGTAACTCCCTGCTCCTGAAATTTCTGCCATGCGACAGATCTGACAGTCCGCGACATA 1235  
 DB 1317 -GGGAACTCCCTGCTCCTGAAATTTCTGCCATGCGACAGATCTGACAGTCCGCGACATA 1375  
 QY 1236 CAGCGGACCCATCTGTCTGACGAGACCTCTGGAACAGAGCTCATGACAGAGTCTCACT 1295  
 DB 1376 CAGCGGACCCATCTGTCTGACGAGACCTCTGGAACAGAGCTCATGACAGAGTCTCACT 1435  
 QY 1296 CTTTAAACCTTTGTGCGGACATCAAAAGTGAAGTCCAGAGCTGTTTCATGTTTCCCTGGG 1355  
 DB 1436 CTTTAAACCTTTGTGCGGACATCAAAAGTGAAGTCCAGAGCTGTTTCATGTTTCCCTGGG 1495  
 QY 1356 AGTGTCTGAGAGCTGAGTACCGGCAAGAAATCAATTCAGGAGCTTTTCCCATGGAAA 1415  
 DB 1496 AGTGTCTGAGAGCTGAGTACCGGCAAGAAATCAATTCAGGAGCTTTTCCCATGGAAA 1555  
 QY 1416 CAACACAGCTTTAGTACAAATGCATCCAGAAATAAAATGSCCTACATCCAAATCTGTC 1475  
 DB 1556 CAACACAGCTTTAGTACAAATGCATCCAGAAATAAAATGSCCTACATCCAAATCTGTC 1615  
 QY 1476 ATCACTCCCAACAGAGAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGGG 1535  
 DB 1616 ATCACTCCCAACAGAGAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGGG 1675  
 QY 1536 CTTAGTAAATGCAAAATACAGGGGTGAGCTTACTATACACACAGCTGCCATCCAGAGGA 1595  
 DB 1676 CTTAGTAAATGCAAAATACAGGGGTGAGCTTACTATACACACAGCTGCCATCCAGAGGA 1735  
 QY 1596 GAAATCTTGGGAGATTTATATGTCATCAACCAAGGTGAACCCAGCTCCAGTCAATG 1655  
 DB 1736 GAAATCTTGGGAGATTTATATGTCATCAACCAAGGTGAACCCAG-----GTCAGATG 1789  
 QY 1656 CTTGAGGTGCTCTGAGTCCCTGAGTCACTGAGTCACTGAGTCTCCAGACATGATCGTACCAC 1715  
 DB 1790 CTTGAGGTGCTCTGAGTCCCTGAGTCACTGAGTCACTGAGTCTCCAGACATGATCGTACCAC 1849  
 QY 1716 TCCCTTTGATGACCATCCCGACTGTGCAGATGTCAGTCTGAGCATTTGGAATATCCA 1775  
 DB 1850 TCCCTTTGATGACCATCCCGACTGTGCAGATGTCAGTCTGAGCATTTGGAATATCCA 1909  
 QY 1776 TTTTAAAGAGAGGACACAGAGGGCAAAATGGGAGGAGTGTGTGAGTGAAGATGAATC 1835  
 DB 1910 TTTTAAAGAGAGGACACAGAGGGCAAAATGGGAGGAGTGTGTGAGTGAAGATGAATC 1969











PI Walke DW, Scoville J;  
 XX WPI; 2004-591302/57.  
 DR P-PSDB; ADR44605.  
 XX  
 PT New isolated human proteins and nucleic acids, useful for diagnosing,  
 PT drug screening, clinical trial monitoring, or treating diseases and  
 PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.  
 XX  
 XX Disclosure; SEQ ID NO 27; 52pp; English.  
 PS  
 XX  
 CC The present invention provides novel human proteins (NHPs) and their  
 CC encoding polynucleotides. The invention is useful for diagnosis, drug  
 CC screening, clinical trial monitoring, treatment of diseases and disorders  
 CC such as cancer and arthritis and cosmetic applications. The invention  
 CC acts as a cytostatic and virucidal agent. The invention is useful in gene  
 CC therapy. The present sequence is a novel human protein (NHP) encoding  
 CC cDNA. The NHP encoding cDNA is located on human chromosome 8.  
 XX  
 CC  
 SQ Sequence 2010 BP; 523 A; 523 C; 484 G; 480 T; 0 U; 0 Other;

Query Match 71.9%; Score 1967; DB 13; Length 2010;  
 Best Local Similarity 98.4%; Pred. No. 0;  
 Matches 2010; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

694 ATGGCAGCCACATCGTGGCTAAGAGGAGAGAGCCTGTGGCCACTGTGTGGTCTACGCG 753  
 1 ATGGCAGCCACATCGTGGCTAAGAGGAGAGAGCCTGTGGCCACTGTGTGGTCTACGCG 60  
 754 GATGGAGCTGGGAAGTGTGGAGCGAATGGTCTGTCAGTCCAGAGTGTGAACATTGG 813  
 61 GATGGAGCTGGGAAGTGTGGAGCGAATGGTCTGTCAGTCCAGAGTGTGAACATTGG 120  
 814 CGGATCCGGAGTGCACAGCACACCCCGAGAAATGGGGCAAAATCTGTGAAGTCTA 873  
 121 CGGATCCGGAGTGCACAGCACACCCCGAGAAATGGGGCAAAATCTGTGAAGTCTA 180  
 874 AGCCAGGATCTGAAACTGCACAGATGGTCTTTGGATCTAGATATAAAACCTCTCAT 933  
 181 AGCCAGGATCTGAAACTGCACAGATGGTCTTTGGATCTAGATATAAAACCTCTCAT 223  
 934 GAAATAAAACCCCAAGCATTTGAGATGGCAGGACATTTGTTGACTCGGCTTTGGGT 993  
 224 -----GCATTGAGATGGCAGGACATTTGTTGACTCGGCTTTGGGT 267  
 994 GTCGCCGTGTCGCCGTGTCAGTCTTGGTCAATTTGGTGTACAGAGCGAGCCAG 1053  
 268 GCTGCCGTGTCGCCGTGTCAGTCTTGGTCAATTTGGTGTACAGAGCGAGCCAG 327  
 1054 AGTGACTATGGCTGGACGTGATGACTCTTCTGCAATGGACGTGGCTTCCAGAGCTTC 1113  
 328 AGTGACTATGGCTGGACGTGATGACTCTTCTGCAATGGACGTGGCTTCCAGAGCTTC 387  
 1114 AACTTCAAAACAGTCCGTCAAGCCAAAGATATCATGGAATTAATGATACAAAGAAATCC 1173  
 388 AACTTCAAAACAGTCCGTCAAGCCAAAGATATCATGGAATTAATGATACAAAGAAATCC 447  
 1174 TTTGGTAACCTCCCTGCTCTGAAATTTGCAATGCAAGCCAGATCTGACAGTGAGCCGACA 1233  
 448 TTTGGTAACCTCCCTGCTCTGAAATTTGCAATGCAAGCCAGATCTGACAGTGAGCCGACA 507  
 1234 TAGAGCGGACCCATCTGTCTGAGGACCTCTGCAAGAGAGTCTATGACAGAGTCTCTCA 1293  
 508 TAGAGCGGACCCATCTGTCTGAGGACCTCTGCAAGAGAGTCTATGACAGAGTCTCTCA 567  
 1294 CTCTTTAACTTTGTCGACATCAAGTCAAGTCCAGAGTCTGTTGTTTCCCTG 1353  
 568 CTCTTTAACTTTGTCGACATCAAGTCAAGTCCAGAGTCTGTTGTTTCCCTG 627  
 1354 GGAGTGTCTGAGAGAGTGTAGTACCGGCAAGAAATCATTTCCAGGACTTTTCCCATGGA 1413  
 628 GGAGTGTCTGAGAGAGTGTAGTACCGGCAAGAAATCATTTCCAGGACTTTTCCCATGGA 687

1414 AACCAACACAGCTTTAGTACAAATGCAATCCAGAAATAAAATGCCCTACATCCAAATCTG 1473  
 688 AACCAACACAGCTTTAGTACAAATGCAATCCAGAAATAAAATGCCCTACATCCAAATCTG 747  
 1474 TCATCACTCCCAACAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGG 1533  
 748 TCATCACTCCCAACAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGG 807  
 1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACACACAGGTGCCATCCAGAG 1593  
 808 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACACACAGGTGCCATCCAGAG 867  
 1594 GAGAATCTTTGGAGATTTATATGTCATCAACCAAGGTGAACCAAGCTCCAGTCAGAT 1653  
 868 GAGAATCTTTGGAGATTTATATGTCATCAACCAAGGTGAACCAAGCTCCAGTCAGAT 927  
 1654 GGCTCTGAGGTGCTCCTGAGTCTCTGAAGTCACTGTGGTCTCTCAGACATGATCGTCACC 1713  
 928 GGCTCTGAGGTGCTCCTGAGTCTCTGAAGTCACTGTGGTCTCTCAGACATGATCGTCACC 987  
 1714 ACTCCCTTTGCAATGACCAATCCGCACCTGTGCAGATGTGAGTCTGAGCATTTGGAATATC 1773  
 988 ACTCCCTTTGCAATGACCAATCCGCACCTGTGCAGATGTGAGTCTGAGCATTTGGAATATC 1047  
 1774 CATTTAAAGAGGACACAGAGGCAAAATGGAGAAAGTGTGATGTGAGTGAAGATGAA 1833  
 1048 CATTTAAAGAGGACACAGAGGCAAAATGGAGAAAGTGTGATGTGAGTGAAGATGAA 1107  
 1834 TCTACATCTGTGACTGCTCTTTTGGACCCCTTTTGGCTGTCTGCTCTGACAGCTTT 1893  
 1108 TCTACATCTGTGACTGCTCTTTTGGACCCCTTTTGGCTGTCTGCTCTGACAGCTTT 1167  
 1894 GGGACCTATGCGTCTGAGAGGCAATCAGACTGTGCGTGAAGCAACTGAAGGTG 1953  
 1168 GGGACCTATGCGTCTGAGAGGCAATCAGACTGTGCGTGAAGCAACTGAAGGTG 1227  
 1954 GGGTTTTTGGTGTGATGCTGTAATCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013  
 1228 GGGTTTTTGGTGTGATGCTGTAATCCCTGGATTACAACTTGAGAGTTTACTGTGTG 1287  
 2014 GACATATACCCCTTTGTGCTTTTTCAGGAAGTGGTTTCAGATGAAGGATCAAGGTGACAG 2073  
 1288 GACATATACCCCTTTGTGCTTTTTCAGGAAGTGGTTTCAGATGAAGGATCAAGGTGACAG 1347  
 2074 CTCCTGGAAGAACCAAAATTTGCTGCAATTTCAAAGGAATACCTTTAGTCTTCAAGATTTCT 2133  
 1348 CTCCTGGAAGAACCAAAATTTGCTGCAATTTCAAAGGAATACCTTTAGTCTTCAAGATTTCT 1407  
 2134 GTCTTTGATATTTCCCTTCTCTGAGAAATTTAAACCAATTTCACTGCTGCCAGGAAGTC 2193  
 1408 GTCTTTGATATTTCCCTTCTCTGAGAAATTTAAACCAATTTCACTGCTGCCAGGAAGTC 1467  
 2194 CGGTTCTCCCGGTGTGTGTCAGTAAACCGGACGCCCTTGCATGTGCTTCTCCCTGGAG 2253  
 1468 CGGTTCTCCCGGTGTGTGTCAGTAAACCGGACGCCCTTGCATGTGCTTCTCCCTGGAG 1527  
 2254 CGTTATACGCCCATACCAACCCAGCTGTCTGCAAAATCTGCAATTCGGAGCTCAAAGGC 2313  
 1528 CGTTATACGCCCATACCAACCCAGCTGTCTGCAAAATCTGCAATTCGGAGCTCAAAGGC 1587  
 2314 CATGAACAGATCTCCCAAGTGCAGACATCAATCTTAGAGAGTGAAGAGAAACCATCACT 2373  
 1588 CATGAACAGATCTCCCAAGTGCAGACATCAATCTTAGAGAGTGAAGAGAAACCATCACT 1647  
 2374 TTCTTCGCAACAGAGGACAGCACTTTTCCCTGCAACAGCTGGCCCCCAAGGCTTTCAAAAT 2433  
 1648 TTCTTCGCAACAGAGGACAGCACTTTTCCCTGCAACAGCTGGCCCCCAAGGCTTTCAAAAT 1707  
 2434 CCTACTCCTATCAGACAGCGGATTTGTGTGTAATTTGATATCCCCCAATGCAAGGCAAG 2493  
 1708 CCTACTCCTATCAGACAGCGGATTTGTGTGTAATTTGATATCCCCCAATGCAAGGCAAG 1767  
 2494 GACTGCGCATGTTAGCAGAAAGAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553

Db	1768	GA	CTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTATCTTATTTGCTACA	1827
Qy	2554	CA	AGTAGCCCATCTGCTGTCAATTGAACTGTGGAGCTGTCATCAGCATGATGGT	2613
Db	1828	CA	AGTAGCCCATCTGCTGTCAATTGAACTGTGGAGCTGTCATCAGCATGATGGT	1887
Qy	2614	GA	CTTGACTCCCTGGCCTGTGGCCTTGAAGAGATTGGGAGGACACACAGAACTCTCA	2673
Db	1888	GA	CTTGACTCCCTGGCCTGTGGCCTTGAAGAGATTGGGAGGACACACAGAACTCTCA	1947
Qy	2674	AA	CTTTCAGATCCCGCTTGATGAAGCCGACTTCAACTACAGAGGGCAAAATGGACTC	2733
Db	1948	AA	CTTTCAGATCCCGCTTGATGAAGCCGACTTCAACTACAGAGGGCAAAATGGACTC	2007
Qy	2734	TAG	2736	
Db	2008	TAG	2010	

Search completed: April 1, 2005, 05:38:18  
Job time : 1388 secs